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<b>(54) Title:</b> PROHORMONE CONVERTASE TRANSFORMED CELLS		
<b>(57) Abstract</b>  Described is the production of mammalian cells expressing prohormone convertase which facilitates the processing of prohormone precursors to active hormones. Also described are variant prohormone convertases, and prohormones. The transformed cells of the present invention may be used in the synthesis of properly processed polypeptide hormones, and in cell culture to reduce dependence upon added hormones and required serum polypeptide factors.		

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## PROHORMONE CONVERTASE TRANSFORMED CELLS

Background of the Invention

5

Field of the Invention

This invention relates to host cells expressing one or more prohormone convertase enzymes and the production of a biologically active polypeptide from these cells. The invention further relates to polypeptide precursor variants having endoprotease cleavage sites which are processed by the host cell.

Description of Related Art

Most, if not all proteinaceous hormones are synthesized as relatively large precursor molecules, prohormones, that are biologically inactive (reviewed in Docherty and Steiner 1982; Loh et al. 1984; Mains et al. 1990). Maturation of the prohormone to its active form often requires endoproteolytic cleavage at paired or multiple basic amino acid residues to liberate the active component from the inactive portion of the precursor molecule. Until recently, almost nothing was known concerning the identity of the proteins responsible for this important stage in processing: the prohormone convertase (PC) enzymes.

Not every kind of cell has the capacity to correctly convert a prohormone to its active mature form through these specific cleavages. For some classes of prohormone this processing is apparently limited to those cells that contain both constitutive and regulated pathways of protein secretion (Gumbiner and Kelly 1982). Cells having both constitutive and regulated pathways of protein secretion are located almost exclusively in the specialized hormone-producing tissues of the endocrine and neuroendocrine systems.

An example of a family of hormones that is processed during regulated secretion is the insulin family of hormones. This family includes insulin, the insulin-like growth factors IGF-I and IGF-II, and relaxin. In their

native environment, all members of this family are synthesized as precursor molecules that require processing to yield active hormone.

When heterologously expressed in cells having only a constitutive pathway of protein secretion, most hormone precursors, such as human preproinsulin, are secreted in an unprocessed prohormone form (Gumbiner and Kelly 1982). Experimental manipulation of mouse AtT-20 cells that disrupted the regulated secretory pathway of those cells has been observed to redirect the polyhormone precursor proopiomelanocortin (POMC) into the constitutive secretory pathway. In that case, POMC was no longer subjected to processing and was found to be secreted from the cell as the intact precursor (Moore et al. 1983). These observations suggest that there is a class of processing enzymes that function only in the regulated pathway of protein secretion; this pathway is apparently limited to certain highly-specialized cell types.

The POMC protein is a prohormone that is subject to differential processing. Expression of mature POMC derivatives is highly tissue-specific; alternate processed forms of the same prohormone precursor are produced in different regions of the brain (Douglass et al. 1984). The enzyme(s) and control mechanisms involved in the generation of this diversity are unknown. The possibility exists that there are tissue-specific enzymes that recognize unique amino acid sites on the prohormone substrate, or alternatively, that only one enzyme is responsible for the endoproteolytic cleavages and is itself under tight metabolic control, with each tissue providing a characteristic intracellular environment that is associated with cleavage at a specific subset of residue pairs.

Until recently, the only known eukaryotic prohormone processing enzyme was the KEX2 gene product of the yeast *Saccharomyces cerevisiae* (Julius et al. 1983 and 1984; Fuller et al. 1989a). The kex2 protein is a serine protease related to the subtilisin family of enzymes and has a preference for specific pairs of basic amino acids on its native hormone precursor substrates (pro-a-factor



maturing type pheromone and the pro-killer toxin). Kex2 shows maximum enzymatic activity at neutral pH with a strict requirement for the presence of calcium (Julius et al. 1984; Fuller et al. 1989a). It is membrane-bound and the mature, active form of the enzyme is localized in the post-Golgi compartment of the yeast cell (Fuller et al. 1989b; Redding et al. 1991). It can effectively serve as a substitute convertase for *bona fide* mammalian PC enzymes when heterologously expressed in otherwise processing-deficient cells by its demonstrated ability to correctly process certain mammalian prohormones: Nerve growth factor, bNGF, in BSC-40 cells (Bresnahan et al. 1990); protein C in baby hamster kidney BHK cells (Foster et al. 1991); POMC both in BSC-40 cells (Thomas et al. 1988) and in COS-1 cells (Zollinger et al. 1990)]. Kex2 was shown to have a highly similar if not identical substrate specificity to the authentic human proalbumin convertase *in vitro* (Bathurst et al. 1986; Brennan et al. 1990). When heterologously expressed in mammalian cells kex2 will home to the post-Golgi compartment, where it is apparently fully active (Germain et al. 1990). These observations have led to speculation that this yeast protein must be both functionally and structurally similar to an authentic mammalian convertase. A search began for the elusive mammalian counterparts of kex2 based upon structural homologies.

#### KEX2 and Fur Hydrophobic Anchor

The Kex2 endoprotease has two hydrophobic regions located at the N-terminal side and C-terminal side. The C-terminal hydrophobic transmembrane anchor is responsible for the anchoring of the Kex2 to a Golgi body of a yeast cell. Deletion of this C-terminal hydrophobic anchor renders the Kex2 endoprotease soluble while still maintaining substrate specificity (EPO PUB No.0327377).

An inspection of genetic data bases identified a potential mammalian homologue of kex2 that shared many features of the active site domain of the kex2 protein: the fur gene product of human liver, furin (Fuller et al. 1989b). Furin was subsequently cloned and successfully

expressed in processing-deficient cells: cotransfection of furin with pro-von Willebrand factor in COS-1 cells (van den Ven et al. 1990; Wise et al. 1990) and with pro-bNGF in African green monkey kidney epithelial BSC-40 cells  
5 (Bresnahan et al. 1990) resulted in correct processing of the precursor substrates.

However, when furin and a prohormone, prorenin, have been coexpressed in mammalian cells, no processing has been observed (Hatsuzawa, et al The Journal of Biological  
10 Chemistry Vol 265 (1990)).

Furin also shared with kex2 a requirement for calcium ions, displayed maximum activity at a neutral pH, and, like kex2, was shown to be a membrane-bound protein in the post-Golgi compartment (Bresnahan et al. 1990). However,  
15 because furin does not seem to be capable of efficiently processing certain hormone precursors such as prorenin, and its mRNA message is apparently expressed in most if not all mammalian cells (Hatsuzawa et al. 1990), the furin protease may play a role in an essential "housekeeping" function in  
20 that it could be responsible for many of the basic amino acid site cleavages occurring in the constitutive secretory pathway of the cell. These functions could be general, or more confined to specific cell-types with the constitutive pathway-dependent processing of growth factors like bNGF.

Because furin does not appear to be directly involved in the endoproteolytic processing of prohormones in endocrine-like tissues, there must be other mammalian proteins both functionally and structurally similar to furin and yeast kex2 that serve as the authentic prohormone  
25 convertases: PC proteins that share distinctive homologies in their active sites. This search for structural homology has recently lead to the discovery of more PC proteins.

By using the technique of "Mixed Oligonucleotides Primed Amplification of cDNA" (MOPAC, Innis 1990), Smeekens  
35 and Steiner (1990) were able to use the conservation of amino acid sequence surrounding the active sites of both bacterial subtilisin and the yeast kex2 protease to amplify a putative prohormone convertase cDNA from human insulinoma. This PC cDNA, termed mPC2, showed an

exceptional degree of homology to the yeast kex2 protease. In similar experiments Seidah and colleagues identified another member of the subtilisin family of proteases, termed, mPC1 (Seidah, et al 1991).

5       The distribution of PC1 and PC2 has so far been observed to be confined to neuroendocrine-derived tissues (Seidah et al. 1990; Seidah et al. 1991; Smeekens et al. 1991), suggesting that these proteins may be candidates for the authentic convertases resident in the regulated  
10       secretory pathways of these tissues. The substrate specificities of PC1 and PC2 for defined pairs of dibasic amino acids at the prohormone cleavage sites do not appear to be identical (Benjannet et al. 1991; Thomas et al. 1991), nor do they share the same pattern of tissue  
15       distribution in the brain (Seidah et al. 1991). This implies that different classes of prohormones may require unique PC enzymes, and that both PC1 and PC2 may be members of a family of specific processing enzymes employed by the endocrine system to generate the diversity of hormones  
20       required throughout the entire organism.

#### **Precursor processing**

      The biosynthetic process begins with the synthesis of the precursor (prepropeptide) on the rough endoplasmic reticulum (RER). The signal peptide (pre-portion) is  
25       clipped off as the proprotein is transported into the cisternae of the RER where protein folding, di-sulfide bond formation and asparagine-linked glycosylation occur (Figure 1). The precursor is then translocated to the Golgi apparatus where more complex glycosylation and  
30       phosphorylation occur. Within the Golgi of some cells, proteins are sorted by an unknown mechanism into two groups: those that will be constitutively secreted and those that undergo regulated secretion. The constitutively secreted proteins will enter vesicles and be transported to  
35       their target continually without the need for any specific stimulus. Proteins undergoing regulated secretion are transported to secretory vesicles and will be released only when an adequate stimulus is provided. Within the secretory vesicles the excision of bioactive peptides from

the larger inactive protein precursors occurs. Two steps involved in this process are endoproteolytic cleavage usually at the carboxyl side of paired basic amino acids (e.g. lys-arg, arg-arg) and exoproteolytic cleavage of flanking basic amino acids by carboxyl- and/or aminopeptidases (reviewed in Mains et al. 1990.).

Many proteins, including NGF (Berger and Shooter 1977), are first synthesized as larger precursor proteins. The function of the precursor is still not well understood. One possible role of the precursor is to aid in protein folding (Steiner 1982, Selby et al. 1987, Wise et al. 1988). The precursor may also direct the protein to the proper location or pathway within the cell as is suggested by Sevarino and colleagues (1989), though this is not the case with the connecting peptide of insulin (Powell et al. 1988, Gross et al. 1990). Additionally, the precursor has been shown to have roles in gamma carboxylation of glutamic acid residues (Pan and Price 1985, Furie and Furie 1988), and regulation of the coordinate synthesis of multiple mature peptides from a single precursor polypeptide eg., POMC. (For review, see Douglass et al. 1984).

#### Relaxin

In the present invention, prorelaxin is used as a typical hormone precursor. The relaxin is first synthesized as a prehormone precursor which undergoes specific processing to form the mature two-chain, disulfide-linked active relaxin. A major part of this processing requires endoproteolytic cleavage at specific pairs of basic amino acid residues. This specific processing does not occur when the precursor is heterologously expressed in cells containing only the constitutive pathway of protein secretion. Mature human relaxin is an ovarian hormonal peptide of approximately 6000 daltons in molecular weight known to be responsible for remodeling the reproductive tract before parturition, thus facilitating the birth process. Hisaw, F.L., Proc. Soc. Exp. Biol. Med., 23:661-663 (1926); Schwabe, C. et al., Biochem. Biophys. Res. Comm., 75: 503-570 (1977); James, R. et al., Nature, 267: 544-546 (1977). This

protein appears to modulate the restructuring of connective tissues in target organs to obtain the required changes in organ structure during pregnancy and parturition. Some of the important roles for relaxin as a pregnancy hormone include inhibition of premature labor and cervical ripening at parturition. While predominantly a hormone of pregnancy, relaxin has also been detected in the non-pregnant female as well as in the male. Bryant-Greenwood, G.D., Endocrine Reviews, 3: 62-90 (1982) and Weiss, G., Ann. Rev. Physiol., 46: 43-52 (1984).

Relaxin consists of two polypeptide chains, referred to as A and B, joined by disulfide bonds with an intra-chain disulfide loop in the A-chain in a manner analogous to that of insulin. Two human genes (H1 and H2) for human relaxin have been identified, and only H2 is expressed in the ovary. Porcine relaxin, the sequence of which has also been determined, has been used in human clinical trials for ripening of the cervix and induction of labor. MacLennan et al., Obstetrics & Gynecology, 68: 598 (1986).

European Pat. Publ. No. 86,649 published Aug. 24, 1983 discloses how to prepare porcine preprorelaxin, porcine prorelaxin, and porcine relaxin. Australian Pat. No. 561,670 issued Aug. 26, 1987, European Pat. Publ. No. 68,375 published January 5, 1983, and Haley et al., DNA, 1: 155-162 (1982) disclose how to prepare porcine relaxin. European Pat. Publ. Nos. 101,309 published Feb. 22, 1984 and 112,149 published June 27, 1984 respectively disclose the molecular cloning and characterization of a gene sequence coding for human relaxin and human H2-relaxin and analogs thereof. U.S. Pat. No. 4,267,101 issued May 12, 1981 discloses a process for obtaining human relaxin from fetal membranes.

#### **Nerve Growth Factor**

Nerve growth factor (NGF), required for sympathetic and sensory neuron survival (Levi-Montalcini and Booker 1960, Gorin and Johnson 1979), is the most well characterized neurotrophic factor in part due to the exceptionally high levels synthesized in the male mouse submaxillary gland. It was from this source that NGF was

purified (Cohen 1960) and its complete amino acid sequence determined (Angeletti 1973). Using this information, Scott and colleagues (1983) identified and cloned the mouse NGF gene by screening a mouse submaxillary gland cDNA library using a probe constructed for a hexapeptide based on the least degenerate codons contained within the NGF sequence. Molecular cloning, using the polymerase chain reaction (PCR) (Saiki et al. 1985, Mullis et al. 1986), has recently revealed that NGF is a member of a family of neurotrophic factors that also includes BDNF (Leibrock et al. 1989) and NT-3 (Hohn et al. 1990, Rosenthal et al. 1990, Maisonpierre et al. 1990a, Ernfors et al. 1990, Jones and Reichardt 1990).

NGF, BDNF and NT-3 are all translated as preproproteins that require endoproteolytic cleavage in order to be active. There is an extensive amount of homology (>50%) between the mature portions of NGF, BDNF, and NT3. However the homologies of the precursor portions are much lower (~20%). The efficiency of processing of the three neurotrophic factors, from their inactive pro-form to the active factor, vary substantially with different cell types.

#### Insulin

Insulin is a polypeptide hormone which is produced in the beta cells of the islets of Langerhans situated in the pancreas of all vertebrates. Insulin is secreted directly into the bloodstream where it regulates carbohydrate metabolism, influences the synthesis of protein and of RNA, and the formation and storage of neutral lipids. The Merck Index, 10th edition, 1983. Insulin promotes anabolic processes and inhibits catabolic ones in muscle, liver and adipose tissue. The structure of human insulin was disclosed in Nature 187,483 (1960). Prior to the discovery of recombinant DNA technology, the major source of insulin for human consumption was the pancreases of slaughtered animals. Human insulin was among the first commercial health care products produced by recombinant technology. A review of the research, development, and recombinant

production of human insulin is in Science 219, 632-637 (1983).

In addition to its role *in vivo*, insulin is also useful in recombinant cell culture. Insulin is an example  
5 of a polypeptide factor important for mammalian cell culture proliferation and anabolism. Some cell cultures produce endogenous insulin and some do not; cell cultures which rely on added insulin are problematic because insulin is unstable in some cultures. European publication number, 0307247A2,  
10 published March 3, 1989, describes the introduction of nucleic acid encoding insulin into a mammalian host cell to eliminate the need for adding exogenous insulin.

Insulin is synthesized as a larger precursor protein, proinsulin. Proinsulin is a single polypeptide chain  
15 containing a sequence of about thirty residues that is absent from mature insulin. Proinsulin, like prorelaxin, has a B-C-A chain structure. The C or connecting peptide joins the carboxyl end of the B chain and the amino terminus of the A chain of the future insulin molecule Biochemistry  
20 3rd edition, pg. 995 (1988). The mature insulin is generated by cleavage of the C peptide at dibasic residues Arg(31)- Arg(32) and Lys(64)-Arg(65). Two distinct processing enzymes have been defined which are specific for their respective dibasic cleavage sites in proinsulin; type  
25 I is substrate specific for the BC junction, while type II is specific for the CA junction (Weiss, Biochemistry 29, 1990).

Naturally occurring mutations in the human insulin gene have been reported by Steiner et al. (Diabetes Care vol.  
30 13, no. 6 pg. 600-609 [1990]). Members of a family with hyperproinsulinemia have a substitution of insulin B chain residue 10, a histidine, with aspartic acid resulting in a proinsulin that is reported to exhibit altered subcellular sorting behavior. In patients having hyperproinsulinemia, a  
35 significant proportion of the newly synthesized Asp-10 proinsulin is secreted from the islets in an unprocessed form via an unregulated or constitutive protein secretory pathway (Steiner et al. PNAS USA, vol. 85, pg. 8943-8947 [1988]) and (Quinn et al. The J. Cell Bio. vol. 113, pg.

987-996 [1991]). Others have shown that insulin containing this B10 H>D mutation results in a more active form of insulin with increased binding to the insulin receptor (Schwartz, et al. PNAS USA vol. 84, pg. 6408-6411 [1987];  
5 Brange et al. Nature vol. 333 pg. 679-682 [1988]; Shoelson et al. vol. Biochem. vol. 31 pg. 1757-1767 [1992]). Brems et al. (Protein Engineering vol. 5 no. 6 pg 519-525 [1992]) report that the replacement of B-chain residue 10, a  
10 histidine, with aspartic acid increased the stability of the insulin. Wild-type human insulin exhibits subunit interactions and forms dimers; dimeric insulin binds to  $Zn^{2+}$  to form hexamers. The histidine residue at position B10 in insulin is involved in co-ordinating zinc ions and it has  
15 been reported by Quinn et al. *Supra*, that the human insulin mutant, B10 histidine to aspartic acid, allows formation of dimers of human proinsulin but not hexamers.  
Insulin Like Growth Factor I and II (IGF-I and IGF-II)

Insulin-like growth factors, or IGFs, by definition  
20 are polypeptides with insulin-like structural and biologic properties which are not neutralized by the presence of excess anti-insulin antibodies. (Endocrinology and Metabolism 2nd ed. [1987]). The complete amino acid sequences of IGF-I and IGF-II have been determined (Rinderknecht, et al Journal  
25 of Biological Chemistry 253 pg. 2769 [1978]; Rinderknecht. et al FEBS Letters 89, 283 [1978]). They are both single-chain polypeptides with three disulfide bridges and a sequence identity of 49 and 47 percent respectively, to human insulin A and B chains. The connecting peptide or C  
30 region is considerably shorter than the one of proinsulin and does not show any significant homology to it. The IGF-I C peptide is not cleaved during the processing to the mature molecule. In addition, IGF-I contains a short, 8 amino-acid, carboxyterminal extension peptide, termed the D  
35 domain, for which no homologous region exists in insulin (Foyt, H.L., Insulin-Like Growth Factors: Molecular and Cellular Aspects [1991])

Both IGF-I and IGF-II are derived from precursors by proteolytic processing (Jansen et al Nature 306, 609



[1984]; Bell, et al Nature 310, 775 [1984]; Jansen et al FEBS letters 179, 243 [1985].

There exists a need for a method of producing polypeptides from their polypeptide precursors in cell culture. It is therefore an object of the present invention to provide host cells that express active prohormone convertases that cleave polypeptide precursors to polypeptides. It is also an object of the present invention to provide a method for the production of a desired polypeptide in cell culture in a manner that results in the proper processing and glycosylation of the desired polypeptide. A related objective of the present invention is the production of polypeptide hormones, such as insulin, relaxin, and IGF-I.

A further object of the present invention relates to providing polypeptide precursor mutants having prohormone convertase cleavage sites for processing by the host cell.

There also exists a need to eliminate problems associated with supplying necessary polypeptide factors (e.g. insulin or transferrin) for the maintenance and growth of recombinant host cells. This need is particularly evident in the use of mammalian cell culture in the production of commercial polypeptides such as pharmaceutical products. It is therefore an object of the present invention to provide mammalian cell cultures that express prohormone convertases that enable processing of polypeptide factor precursors to polypeptide factors needed for mammalian cell culture proliferation and anabolism. It is an object of the present invention to produce polypeptide factors using host cells expressing prohormone convertases.

These and other objects of the invention will be apparent to the ordinary artisan upon consideration of the specification as a whole.

#### Summary of the Invention

The present invention describes a method for the production of a desired polypeptide in host cells expressing a prohormone convertase. In one embodiment the desired polypeptide is a prohormone processed to active

hormone. In another embodiment, the desired polypeptide is any polypeptide factor needed for cell growth or anabolism. In some embodiments, the invention provides polypeptide factor mutants comprising a cleavage site recognizable by a host cell enzyme, such as a prohormone convertase. In a preferred embodiment, a prohormone convertase precursor is provided which is modified to have a host cell cleavage site allowing for processing of the prohormone convertase precursor to active enzyme in the host cell.

10 In one embodiment the host cell constitutively expresses a prohormone convertase. In another embodiment, the host cell is stably transformed with a prohormone convertase.

15 In one aspect of the present invention the production of a heterologous polypeptide factor, such as insulin or transferrin, in a polypeptide factor-dependent host cell is accomplished by a) introducing into the polypeptide factor-dependent host cell nucleic acid encoding a heterologous polypeptide factor precursor comprising a cleavage site recognizable by a host cell enzyme and wherein said host cell is dependent on the cleavage product of said polypeptide factor precursor; and b) culturing said host cell under conditions wherein the polypeptide factor precursor is cleaved at said cleavage site by the host cell enzyme, thereby producing said polypeptide factor.

25 In another aspect of the present invention the production of a desired polypeptide in a host cell expressing a prohormone convertase is accomplished by a) introducing into the host cell nucleic acid encoding a desired polypeptide; and b) culturing said host cell under conditions wherein said desired polypeptide is expressed. Preferably the desired polypeptide is a polypeptide hormone and may be any polypeptide hormone. Preferably, it may be any polypeptide hormone comprised of two or more polypeptide chains. Among the preferred two-chain hormones are insulin, relaxin, and insulin-like growth factors I or II. Among the preferred prohormones are proinsulin, prorelaxin, and precursors of insulin-like growth factors I or II. The prohormone may be a prohormone mutant modified

to contain one or more prohormone convertase cleavage sites. The prohormone or prohormone mutant may be processed by the prohormone convertase in an *in vivo* or *in vitro* manner.

5       The method of producing polypeptide hormones may be further accomplished by inserting into a prohormone, a  
prohormone convertase cleavage site that facilitates  
processing by a prohormone convertase. The preferred  
hormone is a mammalian polypeptide hormone comprised of two  
10 or more polypeptide chains, for example insulin, relaxin,  
insulin-like growth factor I or insulin like growth factor  
II.

In another aspect, the method may be practiced using  
cells transformed to contain a prohormone convertase fused  
15 to a hydrophobic transmembrane Golgi anchor, such as that  
from kex2 or furin.

The present invention discloses nucleic acid (a)  
encoding murine prohormone convertases 1 and 2, (b) mutants  
of prohormone convertase that contain inserted convertase  
20 cleavage sites, and (c) mutants of prohormone convertase  
that contain hydrophobic anchor domains, or heterologous  
pre and prepro sequences from other processed polypeptides.  
Also disclosed are vectors containing such nucleic acid and  
cells expressing such nucleic acid. Methods of effecting  
25 transformation and methods of providing transformed  
mammalian cells are disclosed.

#### Brief Description of the Figures

30   **FIGURE 1**  
AtT20 murine prohormone convertase 1 cDNA (Seq. ID.#1)

**FIGURE 2**  
AtT20 murine prohormone convertase 2 cDNA (Seq. ID #2)

35   **FIGURE 3**  
Murine PC1 amino acid (Seq. ID. #3 )

**FIGURE 4**  
40   Murine PC2 amino acid (Seq.ID. #4)

**FIGURE 5**  
Relaxin dibasic cleavage site mutants

Description of the Preferred EmbodimentsDefinitions

The term "desired polypeptide" refers to any polypeptide intended to be produced in a host cell, but which the host cell either normally does not produce or produces in small amounts, and which is not normally necessary for the continued existence of the cell. Desired polypeptides include a polypeptide having as few as about five amino acids as well as much larger proteins such as factor VIII (2332 amino acids). Desired polypeptides also include any molecule having a pre- or prepro-amino acid sequence, as well as amino acid or glycosylation variants (including natural alleles) capable of exhibiting a biological activity in common with the desired protein. Preferably the polypeptide is heterologous to the host cell in which it is made and is a human polypeptide. Preferred polypeptides are those that have pharmaceutical utility, such as: growth hormones, including human growth hormone, des-N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroid stimulating hormone; thyroxine; insulin; follicle stimulating hormone; calcitonin; leutinizing hormone; glucagon; factor VIII; bombesin; factor IX, thrombin; hemopoietic growth factor; tumor necrosis factor-alpha and -beta; relaxin; mouse gonadotropin-associated peptide; tissue factor protein; inhibin; activin; vascular endothelial growth factor; thrombopoietin; rheumatoid factors; nerve growth factor such as NGF-b; platelet-derived growth factor; fibroblast growth factor such as aFGF and bFGF; epidermal growth factor; transforming growth factor (TGF) such as TGF-alpha and TGF-beta; insulin-like growth factor-I and -II; erythropoietin; osteoinductive factors; an interferon such as interferon-alpha, -beta, and -gamma; nerve growth factor (NGF), BDNF, and NT-3; colony stimulating factors (CSFs), e.g., M-CSF, GM-CSF, and G-CSF; interleukins (ILs), e.g., IL-1, IL-2, IL-3, IL-4, etc.; decay accelerating factor; atrial natriuretic peptides A, B or C; and fragments of any of the above-listed polypeptides. In addition, one or more predetermined amino acid residues in the polypeptide may be

substituted, inserted, or deleted, for example, to produce products with improved biological properties, or to vary expression levels, such as adding or deleting a dibasic amino acid site susceptible to cleavage by host cell enzyme. Some of the desired polypeptides falling within this present invention may optionally possess covalent or non-covalent modifications of features of a naturally occurring molecule, for example, glycosylation modifications.

10 "Desired polypeptide precursor mutant" refers to a desired polypeptide precursor comprising a non-naturally occurring enzyme cleavage site as well as a desired polypeptide precursor mutant optionally having amino acid substitutions, deletions, and/or insertions at certain  
15 other positions provided that the final construct possesses the desired activity. The desired polypeptide precursor mutants of the present invention also include those mutants wherein glycosylation or other features of a naturally occurring molecule have been modified covalently or non-  
20 covalently provided that the final mutant construction possesses the desired activity.

As used herein, "polypeptide factor," refers to any protein necessary for the survival or growth of a host cell in culture. The polypeptide factor may be a hormone,  
25 growth factor, peptide hormone, autocrine factor, transport protein, oncogene/proto-oncogene and the like. Examples of polypeptide factors that are hormones are, for example, insulin, follicle stimulating hormone (FSH), calcitonin, leutinizing hormone (LH), glucagon, parathyroid hormone  
30 (PTH), thyroid stimulating hormone (TSH), thyroid releasing hormone (TRH), and growth hormone. Additional examples of polypeptide factors are the transport proteins, such as, transferrin, serum albumin, ceruloplasmin, low density lipoprotein (LDL) and high density lipoprotein (HDL). Some  
35 polypeptide factors, often are described as autocrine because, in some instances, the cells they are secreted from can respond to the secreted factor; example of such factors are interleukin-2, epidermal growth factor (EGF), fibroblast growth factor (FGF), thrombin, nerve growth

factor, hemopoietic growth factor and granulocyte-macrophage colony stimulating factor (GM-CSF). Yet other examples of polypeptide factors are peptides resulting from the expression of certain oncogenes/proto-oncogenes. The proteins encoded by these proto-oncogenes encompassed by the polypeptide factors of this invention are growth factors, transducing proteins and membrane receptors. Examples of a growth factor is PDGF (b subunit) encoded by the sis oncogene. Examples of peripheral membrane proteins are the truncated cell surface receptor for EGF encoded by erb-B, the cell surface receptor for M-CSF/CSF-1 encoded by fms and the receptors encoded by neu and ros. An example of a transducing protein is tyrosine kinase at the inner surface of the plasma-membrane encoded by abl. While these polypeptide factors are typically not added to a culture medium, they may be substituted for another polypeptide factor. The definition of polypeptide factor includes amino acid mutants which maintain the functional characteristics of the polypeptide factor. These mutants may comprise one or more amino acid differences in the overall sequence and may be prepared by deletions, substitutions, and/or insertions of one or more amino acids in the overall sequence. Through the use of recombinant DNA technology polypeptide factor mutants may be prepared by altering the underlying DNA. All such variations or alterations in the structure of a polypeptide factor mutant is included within the scope of this invention so long as the functional activity is maintained.

"Polypeptide factor precursor mutant" refers to a polypeptide factor precursor comprising a non-naturally occurring enzyme cleavage site.

"Polypeptide factor-dependent host cell" refers to a host cell requiring one or more polypeptide factors in the culture medium for growth or survival. The polypeptide factor(s) for a particular host cell is determined using general methods known to the ordinarily skilled artisan.. Elimination of the polypeptide factor from the medium may result in death of the cell or in inhibited growth.

"Heterologous polypeptide factor" is defined as a polypeptide factor not naturally occurring in the host cell.

A "heterologous" element is defined herein to mean foreign to the cell, or (unless otherwise specified) homologous to the cell but in a position within the host cell in which the element is ordinarily not found. An "endogenous" element is defined herein to mean naturally occurring in the cell. An "endogenous host cell enzyme" is defined to mean an enzyme which is endogenous to the cell.

10 "Prohormone" refers to a hormone precursor.

"Prohormone convertase" enzymes are specialized proteinases having conserved active site domains which are substrate specific and cleave exclusively at certain sets of basic residues, preferably Lys-Arg, Arg-Arg, Lys-Lys and Arg-Lys. This type of proteinase is responsible for processing large precursor proteins, such as prorelaxin, to their biologically active form. In the present invention prohormone convertase is used to refer to mammalian PC1 and PC2, furin, and includes mammalian, yeast, or any prohormone convertase that is biologically active as described above. The yeast enzyme, Kex2, is specifically excluded from the definition of prohormone convertase enzymes. In the present invention "prohormone convertase cleavage site" refers to a cleavage site recognized by a prohormone convertase.

25 "Basic residue" refers to amino acids in which the R groups have a net positive charge at pH 7.0, for example: Lysine, Arginine, Histidine.

"Dibasic cleavage site" contains two amino acids with basic charges on their side chains that are specifically cleaved by prohormone convertases, the preferred amino acids are Lys-Arg, Arg-Arg, Lys-Lys and Arg-Lys.

4 "Kex2" refers to a Saccharomyces yeast endoprotease which specifically processes a mating type factor and a killer factor. Kex2 contains an amino terminal catalytic domain followed by a cysteine-rich region, a transmembrane domain, and a short cytoplasmic tail.

"Furin" refers to a protein encoded by the gene fur which has homology to the Kex2 protein and is involved in processing of protein precursors. Furin is expressed

constitutively in most cell types including CHO, HepG2, PC12, BHK and in most tissue. Furin mediates basic cleavages which occur in the Golgi, and has a preference for cleaving Lys-Arg residues. Like Kex2, human furin contains  
5 an amino terminal catalytic domain followed by a cysteine-rich region, a transmembrane domain, and a short cytoplasmic tail.

"Mammalian PC1 (mPC1)" refers to the sequence identified in Fig 4, and all mammalian prohormone  
10 convertases having equal to or greater than 95% homology to the sequence in Fig. 4.

"Mammalian PC2 (mPC2)" refers to the sequence identified in Fig.5 and all mammalian prohormone convertases having equal to or greater than 95% homology to the sequence  
15 in Fig 5.

A "cleavage site recognizable by a host cell enzyme" refers to the cleavage site of an enzyme naturally occurring in a host cell. The preferred naturally occurring enzyme of the present invention is a prohormone convertase.

"Prohormone convertase precursor mutant" refers to a  
20 prohormone convertase precursor comprising a non-naturally occurring enzyme cleavage site as well as desired polypeptide precursor mutants optionally having substitutions, deletions, and/or insertions at certain other  
25 positions provided that the final construct possesses the desired activity.

"Precursor" means a form of the protein which may be converted into the desired protein by processing. It may be a natural pro-form or prepro-form of the protein, or a  
30 synthetic pro-form wherein a gene coding for the desired protein is preceded by a heterologous signal, or leader sequence, and such as constructs which are routinely produced *in vitro*.

An "Isolated" polypeptide means polypeptide which has  
35 been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the polypeptide, and may include proteins, hormones, and other



substances. In some embodiments, the polypeptide will be purified (1) to greater than 95% by weight of protein as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-Terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE using Coomassie blue or, preferably, silver stain. This definition specifically includes polypeptides present in situ in a host cell wherein the host cell in its native form lacks the polypeptide. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step. In preferred embodiments, isolated prohormone convertase is utilized.

"Nucleic acid" refers to a nucleotide sequence comprising a series of nucleic acids in a 5' to 3' phosphate diester linkage that may be either an RNA or a DNA sequence. If DNA, the nucleotide sequence is either single or double stranded. Polypeptide-encoding nucleic acid is RNA or DNA that encodes a biologically or antigenically active polypeptide, is complementary to nucleic acid sequence encoding such polypeptide, or hybridizes to nucleic acid sequence encoding such polypeptide and remains stably bound to it under stringent conditions.

"Isolated" polypeptide nucleic acid is a nucleic acid that is identified and separated from at least one contaminant nucleic acid with which it is ordinarily associated in the natural source of the nucleic acid. Isolated nucleic acid is other than in the form or setting in which it is found in nature. Isolated prohormone convertase nucleic acid therefore distinguishes prohormone convertase nucleic acid as it exists in natural cells. However, isolated prohormone convertase nucleic acid includes prohormone convertase in ordinarily prohormone convertase-expressing cells where the nucleic acid is, for example, in a chromosomal location different from that of natural cells.

"Hydrophobic transmembrane anchor" is the hydrophobic region of enzymes localized in the golgi, RER or other cellular membranes which facilitates localization of the enzyme in that region and reduces the loss of enzyme from the cell, specifically illustrating such anchors are the kex2 and furin transmembrane anchors.

The term "mutant" as used herein is defined as a molecule in which the amino acid sequence, glycosylation, or other feature of a naturally occurring molecule has been modified covalently or noncovalently and is intended to include variants. Some of the variants falling within this invention possess amino acid substitutions or additions of a host cell enzyme cleavage sites and optionally also substitutions, deletions, and/or insertions at certain other positions provided that the final construct possesses the desired activity.

The term "host cell" refers to those cells capable of growth in culture and capable of expressing a prohormone convertase, and / or a desired protein and/or a polypeptide factor(s). The host cells referred to in this disclosure encompass cells in *in vitro* culture as well as cells that are within a host animal. While the preferred host cells in *in vitro* culture of this invention are mammalian cells, other cells may be used. Some of the embodiments of this invention involve the use of a host cell enzyme which itself requires processing from a precursor to an active form; for those host cells, such as bacterial or yeast, that lack the enzyme required to process the host cell enzyme, such enzyme may be introduced into the host cell to facilitate practice of the methods of this invention.

The expressions "cell," and "cell culture" are used interchangeably and all such designations include progeny and ancestors. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same function or biological activity as screened for in the cell are included. Where distinct designations are intended, it will be clear from the context.

"Transfection" refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan for example,  $\text{CaPO}_4$  and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

"Transformation" means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook et al., *supra*, is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., *Gene*, 23: 315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method described in sections 16.30-16.37 of Sambrook et al., *supra*, is preferred. General aspects of mammalian cell host system transformations have been described by Axel in U.S. 4,399,216 issued 16 August 1983. Transformations into yeast are typically carried out according to the method of Van Solingen et al., *J. Bact.*, 130: 946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76: 3829 (1979). However, other methods for introducing DNA into cells such as by nuclear injection, electroporation, or by protoplast fusion may also be used.

"Stably transformed host cell" refers to a cell wherein the inserted nucleic acid is present either integrated in the host cell or extrachromosomally, and wherein the inserted nucleic acid is continuously produced by the cell for about two weeks after insertion of nucleic acid. General aspects of mammalian cell host system transformations have been described by Axel in U.S. 4,399,216 issued 16 August 1983.

The term "medium" refers to the aqueous environment in which the mammalian cells are grown in culture. The medium comprises the physiochemical, nutritional, and hormonal environment. Traditionally the medium has been formulated by the addition of nutritional and growth factors necessary for growth or survival. "Serum-free medium" refers to a medium lacking serum. The hormones, growth factors, transport proteins, peptide hormones and the like typically found in serum which are necessary for the survival or growth of particular cells in culture are typically added as a supplement to serum-free medium. A "defined medium" refers to a medium comprising nutritional and hormonal requirements necessary for the survival and growth of the cells in culture such that the components of the medium are known. A defined medium provided by the method of the instant invention establishes a local environment for a particular host cell that may differ from the general environment of the medium. Cells in serum-free medium generally require insulin and transferrin for optimal growth. These two factors should be tested first when determining what factors a given cell requires. Most cell lines require one or more of the growth factors. These include epidermal growth factor (EGF), fibroblast growth factor (FGF), insulin-like growth factors I and II (IGF-I, IGF-II), nerve growth factor (NGF), etc. Other classes of factors which may be necessary include: transport and binding proteins (e.g., ceruloplasmin, high and low density lipoprotein [HDL, LDL], albumin); and hormones.

"Stringent conditions" are those hybridization conditions that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% NaDodSO<sub>4</sub> at 50° C; (2) employ during hybridization a denaturing agent such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42° C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x

Denhardt's solution, sonicated salmon sperm DNA (50 g/ml), 0.1% SDS, and 10% dextran sulfate at 42 C, with washes at 42 C in 0.2 x SSC and 0.1% SDS.

"Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the digest on polyacrylamide or agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. This procedure is known generally. For example, see Lawn et al., Nucleic Acids Res., 9: 6103-6114 (1981), and Goeddel et al., Nucleic Acids Res. 8: 4057 (1980).

"Polymerase chain reaction," or "PCR," as used herein generally refers to a procedure wherein minute amounts of a specific piece of nucleic acid, RNA and/or DNA, are amplified as described in U.S. Pat. No. 4,683,195 issued 28 July 1987. Generally, sequence information from the ends of the region of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will be identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers may coincide with the ends of the amplified material. PCR can be used to amplify specific RNA sequences, specific DNA sequences from total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage or plasmid sequences, etc. See generally Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51: 263 (1987); Erlich, ed., PCR Technology, (Stockton Press, NY, 1989). As used herein, PCR is considered to be one, but not the only, example of a nucleic acid polymerase reaction method for amplifying a nucleic acid test sample, comprising the use of a known nucleic acid as a primer and utilizing a nucleic acid polymerase to amplify or generate a specific piece of nucleic acid.

"Oligonucleotide-mediated mutagenesis" refers to a method for preparing substitution, deletion, and insertion mutants of prohormone convertase 1 or 2 encoding DNA. This

technique is well known in the art as described by Adelman et al., DNA, 2: 183 (1983). Briefly, the prohormone convertase 1 or 2 DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the prohormone convertase 1 or 2. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the prohormone convertase 1 or 2. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (Proc. Natl. Acad. Sci. USA, 75: 5765 [1978]).

"Glycosylation" refers to the post-translational modification process of adding a series of sugar residues to proteins to produce glycoproteins. Glycosylation can occur in the cytosol, the endoplasmic reticulum, or the Golgi apparatus of mammalian cells.

"pRK5" and "pRK7" are expression vectors used to transform mammalian cells. The construction of expression vector pRK5 was described in European Patent Application 0307247A2, published March 15, 1989. The pRK7 vector was described in European Patent Application 278,776 published August 17, 1988.

"Regulated protein secretory pathway" refers to the cellular pathway for exocytosis which is regulated over short periods of time by physiological stimuli, such as cyclic AMP. This pathway is not required for cell viability and is only present in specialized secretory cells such as endocrine and exocrine cells.

"Constitutive protein secretory pathway" refers to the unregulated cellular pathway which is found in cells such as macrophages and fibroblasts.

"Human insulin" refers to a protein exhibiting a biological activity in common with naturally occurring human insulin. Human insulin biological activity includes promoting glucose utilization, protein synthesis, and the formation and storage of neutral lipids. "Human proinsulin" is defined to be a molecule containing the B, C, and A chain amino acid sequence and includes amino acid variants that maintain the functional characteristics of insulin discussed above. These variants may comprise one or more amino acid differences in the overall sequence and may be prepared by deletions, substitutions, and/or insertions of one or more amino acids in the overall sequence. Through the use of techniques common in the field, human proinsulin mutants may be prepared by altering the protein itself or the nucleic acid encoding the protein. All such variations or alterations in the structure of human proinsulin resulting in human proinsulin variants are included within the scope of this invention so long as the functional activity of proinsulin is maintained.

"Human relaxin" denotes a functional protein capable of exhibiting a biological activity. Human relaxin biological activity is defined as any of 1) immunological cross-reactivity with at least one epitope of human relaxin or 2) the possession of a least one hormonal function in common with human relaxin. "Human prorelaxin" is defined to be a molecule containing the B, C, and A chain amino acid sequence and includes amino acid variants which maintain the functional characteristics discussed above. These variants may comprise one or more amino acid differences in the overall sequence and may be prepared by deletions, substitutions, and/or insertions of one or more amino acids in the overall sequence. Through the use of recombinant DNA technology human prorelaxin mutants may be prepared by altering the underlying DNA. All such variations or alterations in the structure of human

prorelaxin resulting in human prorelaxin variants are included within the scope of this invention so long as the functional activity is maintained.

As used herein, "IGF-I" refers to IGF-I from any species, including bovine, ovine, porcine, equine, and preferably human, in naturally occurring-sequence or in variant form, or from any source, whether natural, synthetic, or recombinant. Variants may comprise one or more amino acid differences in the overall sequence and may be prepared by deletions, substitutions, and/or insertions of one or more amino acids in the overall sequence. All such variations or alterations in the structure of IGF-I resulting in human prorelaxin variants are included within the scope of this invention so long as the functional activity is maintained.

#### Use of Prohormone Convertase in Mammalian Cell Culture

In the present invention, the host cells expressing a prohormone convertase may be used to express polypeptide factors needed for cell growth and anabolism.

Mammalian cells frequently require one or more hormones from each of the following groups: steroids, prostaglandins, growth factors, pituitary hormones, and polypeptide hormones. Most cell types require insulin to survive in serum-free media. (Sato, G.H. et al. in Growth of Cells in Hormonally Defined Media, [Cold Spring Harbor Press, N.Y., 1982]). In addition to the hormones, cells may require transport proteins such as transferrin (plasma iron transport protein), ceruloplasmin (a copper transport protein), and high density lipoprotein (a lipid carrier) to be added to cell media. The set of optimal hormones or transport proteins will vary for each cell type. Most of these hormones or transport proteins have been added exogenously or, in a rare case, a mutant cell line has been found which does not require a particular factor.

Cellular proliferation has been studied to elaborate the events necessary to lead from quiescent growth arrest to the cellular commitment to proliferate. Various polypeptide factors have been found to be involved in that



transformation. These transformed cells have been found to produce peptide growth factors in culture. (Kaplan, P.L. et al., PNAS 79:485-489 [1982]). The secretion from a cell of a factor to which that same cell can respond has been referred to as an "autocrine" system. Numerous factors have been described as autocrine: bombesin, interleukin-2 (Duprez, V. et al. PNAS 82:6932 [1985]); insulin, (Serrero, G. In Vitro Cellular & Dev. Biol. 21[9]:537 [1985]); transforming growth factor alpha (TGF-a), platelet-derived growth factor (PDGF); transforming growth factor-beta (TGF-b), (Sporn, M.B. & Roberts, A.B., Nature 313:745 [1985]); sarcoma growth factor (SGF), (Anzano, M.A. et al., PNAS 80:6264 [1983]); and, hemopoietic growth factor, granulocyte-macrophage colony stimulating factor (GM-CSF), (Lang, R.A. et al., Cell 43:531 [1985]). The methods of the present invention are suitable for cells expressing one or more prohormone convertases and further comprising nucleic acid encoding a polypeptide factor required for proliferation or for maintenance of cellular integrity. In the present invention the preferred polypeptide factor is insulin.

In the present invention, the host cells expressing a prohormone convertase may be used to express any desired polypeptide which requires processing from a precursor form. The cells of the present invention may be used in cell culture to produce any polypeptide of interest even those not requiring processing by a prohormone convertase.

In the present invention nucleic acid encoding a prohormone convertase may be introduced prior to the introduction of nucleic acid encoding a desired polypeptide or a polypeptide factor. In the present invention, nucleic acid encoding a prohormone convertase may be introduced simultaneously with nucleic acid encoding a desired polypeptide or a polypeptide factor wherein the nucleic acid may be on the same or separate vectors.

As described more fully herein, the present invention describes a method for the production of a heterologous polypeptide factor in a polypeptide factor-dependent host cell comprising a) introducing into the polypeptide factor-

dependent host cell nucleic acid encoding a heterologous polypeptide factor precursor comprising a cleavage site recognizable by a host cell enzyme and wherein said host cell is dependent on the cleavage product of said polypeptide factor precursor; and b) culturing said host cell under conditions wherein the polypeptide factor precursor is cleaved at said cleavage site by the host cell enzyme, thereby producing said polypeptide factor. Optionally polypeptide factor is recovered.

10 The present invention further describes a method for the production of a desired polypeptide in a host cell expressing a prohormone convertase comprising a) introducing into the host cell expressing said prohormone convertase nucleic acid encoding a desired polypeptide; and  
15 b) culturing said host cell under conditions wherein said desired polypeptide is expressed. Optionally the desired polypeptide is recovered.

For any of the cleavage events described herein, additional host cell enzyme or heterologous enzyme is added to the host cell as desired.

20 The present invention discloses nucleic acid encoding a polypeptide factor precursor mutant comprising an prohormone convertase cleavage site. Another aspect of the present invention is a nucleic acid encoding a prohormone  
25 convertase that is joined to nucleic acid encoding a hydrophobic transmembrane anchor. This joined nucleic acid directs the synthesis of a polypeptide fusion product wherein the catalytically active prohormone convertase is covalently attached to a hydrophobic transmembrane anchor.  
30 Among the preferred hydrophobic transmembrane anchors are the KEX2 hydrophobic transmembrane anchor and the furin hydrophobic transmembrane anchor.

The present invention also provides for a prohormone convertase precursor mutant having nucleic acid encoding a  
35 prohormone convertase cleavage site.

The present invention further provides for host cells having nucleic acid encoding a polypeptide factor precursor mutant comprising a prohormone convertase cleavage site.

The nucleic acid and methods disclosed herein are suitable for use for expression in a wide range of host cell lines. Mammalian cells are the preferred host cell for expressing prohormone convertases. The host cell of  
5 the present invention may be a mammalian cell that does not normally express detectable amounts of prohormone convertase. In addition, the mammalian cell of the present invention may be a mammalian cell that produces levels of prohormone convertase that are insufficient to process the  
10 desired polypeptide precursor to desired polypeptide. Transformation of such cells by nucleic acid encoding a prohormone convertase results in an increase in prohormone convertase sufficient to process desired polypeptide precursor to polypeptide.

#### 15 Isolation of Nucleic Acid

The nucleic acid encoding the prohormone, convertase, or other polypeptide of interest may be obtained from any cDNA library prepared from tissue or cells believed to possess the polypeptide mRNA and to express it at a  
20 detectable level. The desired gene may also be obtained from a genomic library.

Libraries are screened with probes designed to identify the gene of interest or the protein encoded by it. For cDNA expression libraries, suitable probes include  
25 monoclonal or polyclonal antibodies that recognize and specifically bind to the desired polypeptide; oligonucleotides of about 20-80 bases in length that encode known or suspected portions of the polypeptide of interest's cDNA from the same or different species; and/or  
30 complementary or homologous cDNAs or fragments thereof that encode the same or a similar gene. Appropriate probes for screening genomic DNA libraries include, but are not limited to, oligonucleotides; cDNAs or fragments thereof that encode the same or a similar gene; and/or homologous  
35 genomic DNAs or fragments thereof. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures as described in chapters 10-12 of Sambrook et al., supra.

An alternative means to isolate the gene encoding the

polypeptide of interest is to use polymerase chain reaction (PCR) methodology as described in section 14 of Sambrook et al., supra. This method requires the use of oligonucleotide probes that will hybridize to the gene of interest.

5 Strategies for selection of oligonucleotides are described below.

Another alternative method for obtaining the gene of interest is to chemically synthesize it using one of the methods described in Engels et al. (Agnew. Chem. Int. Ed. Engl., 28: 716-734 [1989]). These methods include

10 triester, phosphite, phosphoramidite and H-Phosphonate methods, PCR and other autoprimer methods, and oligonucleotide syntheses on solid supports. These methods may be used if the entire nucleic acid sequence of the gene

15 is known, or the sequence of the nucleic acid complementary to the coding strand is available, or alternatively, if the target amino acid sequence is known, one may infer potential nucleic acid sequences using known and preferred coding residues for each amino acid residue.

20 A preferred method of practicing this invention is to use carefully selected oligonucleotide sequences to screen cDNA libraries from various tissues, depending on the source of the gene or polypeptide of interest.

The oligonucleotide sequences selected as probes

25 should be of sufficient length and sufficiently unambiguous that false positives are minimized. The actual nucleotide sequence(s) is usually based on conserved or highly homologous nucleotide sequences or regions of other polypeptides homologous to the polypeptide of interest.

30 The oligonucleotides may be degenerate at one or more positions. The use of degenerate oligonucleotides may be of particular importance where a library is screened from a species in which preferential codon usage in that species is not known. The oligonucleotide must be labeled such

35 that it can be detected upon hybridization to DNA in the library being screened. The preferred method of labeling is to use 32-P labeled ATP with polynucleotide kinase, as is well known in the art, to radiolabel the oligonucleotide. However, other methods may be used to

label the oligonucleotide, including, but not limited to, biotinylation or enzyme labeling.

Of particular interest is prohormone convertase nucleic acid that encodes a full-length polypeptide. In some preferred embodiments, the nucleic acid sequence includes the prohormone convertase signal sequence. Nucleic acid having all the protein coding sequence is obtained by screening selected cDNA or genomic libraries, and, if necessary, using conventional primer extension procedures as described in section 7.79 of Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

In preferred embodiments of this invention DNA hybridization probes are used to identify novel prohormone convertase candidate enzyme messages in cell lines containing regulated secretory pathways. The murine pituitary tumor cell line AtT-20 is suitable because it is neuroendocrine-derived, and secretes ACTH. It would therefore be expected to contain processing enzymes involved in the conversion of the prohormone proopiomelanocortin (POMC) precursor to mature ACTH, a process which requires cleavage at specific pairs of basic amino acids in the prohormone substrate.

Candidate cDNAs expressed in the AtT-20 cells may be amplified by the MOPAC procedure (Innis 1990) using degenerate primer sequences based on those of Smeekens and Steiner (1990). In particularly preferred embodiments, two PC-like cDNAs are amplified and cloned from the AtT-20 cells: mPC2 (greater than 95% homologous to the human PC2 of Smeekens and Steiner) and second sequence similar to mPC2, termed mPC1.

#### Construction of polypeptide mutants

Amino acid sequence variants of the prohormone convertase, polypeptide factor, desired polypeptide or other polypeptide of interest are prepared by introducing appropriate nucleotide changes into the encoding DNA, or by in vitro synthesis of the desired polypeptide. Such variants include, for example, deletions from, or insertions or substitutions of, residues within the amino

acid sequence for the polypeptide of interest. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the polypeptide, such as changing the number or position of glycosylation sites, altering the membrane anchoring characteristics, and/or altering the intracellular location of the polypeptide by inserting, deleting, or otherwise affecting the leader sequence of the naturally occurring polypeptide of interest.

In designing amino acid sequence polypeptide variants, the location of the mutation site and the nature of the mutation will method of labeling is to use 32-P labeled ATP with polynucleotide kinase, as is well known in the art, to radiolabel the oligonucleotide. However, other methods may be used to label the oligonucleotide, including, but not limited to, biotinylation or enzyme labeling, substituting first with conservative amino acid choices and then with more radical selections depending upon the results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

There are two principal variables in the construction of amino acid sequence variants: the location of the mutation site and the nature of the mutation. In general, the location and nature of the mutation chosen will depend upon the characteristic to be modified.

Amino acid sequence deletions generally range from about 1 to 30 residues, more preferably about 1 to 10 residues, and typically are contiguous. Deletions may be introduced into regions of low homology between the polypeptide of interest and other polypeptides to modify the activity of the polypeptide of interest. Deletions from the polypeptide of interest in areas of substantial homology with any other polypeptide will be more likely to modify the biological activity of the polypeptide of interest more significantly. The number of consecutive deletions will be selected so as to preserve the tertiary

structure of polypeptide of interest in the affected domain, e.g., beta-pleated sheet or alpha helix.

Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one  
5 residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions (i.e., insertions within the sequence of the polypeptide of interest) may range generally from about 1 to 10 residues,  
10 more preferably 1 to 5, most preferably 1 to 3. An example of a terminal insertion is an N-terminal methionyl residue, an artifact of the direct expression of a polypeptide in bacterial recombinant cell culture.

Other insertional variants of the polypeptide of  
15 interest include the fusion to the N- or C-terminus of the polypeptide of immunogenic polypeptides, e.g., bacterial polypeptides such as beta-lactamase or an enzyme encoded by the E. coli trp locus, or yeast protein, and C-terminal fusions with proteins having a long half-life such as  
20 immunoglobulin constant regions (or other immunoglobulin regions), albumin, or ferritin, as described in WO 89/02922 published 6 April 1989.

Another group of variants are amino acid substitution variants. These variants have at least one amino acid  
25 residue in the polypeptide of interest removed and a different residue inserted in its place. The sites of greatest interest for substitutional mutagenesis include sites identified as the active site(s) of the polypeptide of interest, and sites where the amino acids found in  
30 homologous polypeptides from various species are substantially different in terms of side-chain bulk, charge, and/or hydrophobicity.

DNA encoding amino acid sequence variants of the beta-8 integrin subunit is prepared by a variety of methods  
35 known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of

an earlier prepared variant or a non-variant version of the beta-8 integrin subunit. These techniques may utilized beta-8 integrin subunit nucleic acid (DNA or RNA), or nucleic acid complementary to the beta-8 integrin subunit  
5 nucleic acid. In the present invention, the site-directed mutagenesis method of Kunkel, Methods of Enzymology 154:367-383, 1987 are particularly preferred.

Another method for preparing the prohormone convertase mutants of this invention are preferably constructed by  
10 mutating the nucleic acid sequences that encode the native prohormone convertase. Generally, particular regions or sites of the nucleic acid will be targeted for mutagenesis, and thus the general methodology employed to accomplish this is termed site-directed mutagenesis. In the present  
15 invention the preferred method of site-directed mutagenesis is by the method of Kunkel (Methods of Enzymology 154:367-382, 1987).

Another method for preparing mutants of this invention is by oligo-mediated mutagenesis. Oligonucleotide-mediated  
20 mutagenesis is a preferred method for preparing substitution, deletion, and insertion mutants of prohormone convertase 1 or 2 encoding DNA. This technique is well known in the art as described by Adelman et al., DNA, 2: 183 (1983). Briefly, the prohormone convertase 1 or 2 DNA  
25 is altered by hybridizing an oligonucleotide encoding the desired mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or naturally occurring DNA sequence of the prohormone convertase 1 or 2. After  
30 hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the prohormone convertase 1 or 2.

35 Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will



hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (Proc. Natl. Acad. Sci. USA, 75: 5765 [1978]).

5        PCR mutagenesis is also suitable for making amino acid mutants. While the following discussion herein may refer to DNA, it is understood that the technique also finds application with RNA. The PCR technique refers to the procedure outlined in Genetic Engineering Vol 12 pp 115-137,  
10 [1990] by Arnheim; Analytical Chemistry, vol 62 pp 1202-1214 [1990] by Gibbs; and Science vol 252 pp. 1643-1651 [1991] by Gelfand

#### Mutants Affecting Polypeptide precursor processing

One aspect of the present invention is a polypeptide  
15 factor precursor mutant containing modification within the nucleic acid encoding pre-pro or pro sequence which optimizes the precursor processing by the prohormone convertase. Cells vary widely in their processing capability, and consequently, in the prohormone maturation  
20 products that are ultimately secreted from them. This difference in processing of polypeptide factor precursor mutants could be the result of several factors: (a) the precursor sequence itself could influence the accessibility of the prohormone convertase to the cleavage site, (b) each  
25 specific pattern could represent a distinctly different processing enzyme, (c) there could be a limited number of prohormone convertases that exhibit specificity due to their location (microenvironment) or relative abundance within the cell, (d) similar precursors could be modified  
30 in the various cell types influencing their accessibility to the prohormone convertase.

In the present invention, one preferred polypeptide factor precursor mutant is a human proinsulin mutant having a prohormone convertase cleavage site wherein the cleavage  
35 site is processed in the constitutive pathway of the host cell. The preferred proinsulin variant is one comprising a residue substitution for naturally occurring residues in the Type I and/or Type II cleavage sites as outlined:

Proinsulin residue Lys 29 is substituted with any of a residue selected from the group of Arg, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Arg.

5 Proinsulin residue Arg 31 is substituted with any of a residue selected from the group of Lys, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Lys.

10 Proinsulin residue Leu 62 is substituted with any of a residue selected from the group of Arg, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Lys, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Lys or Arg.

15 Site-directed mutagenesis by the method of Kunkel (Kunkel 1987) is a preferred method for preparing substitution, deletion, and insertion variants of polypeptide precursors.

A preferred mammalian prohormone convertase 1 (mPC1) precursor mutant comprises a residue substitution for naturally occurring residues in the prohormone convertase cleavage site of the precursor as outlined: mPC1 precursor residue Lys 80 is substituted with any of a residue selected from the group Arg, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Arg.

25 A preferred mammalian prohormone convertase 2 (mPC2) precursor mutant comprises a residue substitution for naturally occurring residues in the prohormone convertase cleavage site of the precursor as outlined. mPC2 precursor residue Lys 77 is substituted with any of a residue selected from the group Arg, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Arg. mPC2 precursor residue Arg 78 is substituted with any of a residue selected from the group Lys, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Ala. mPC2 precursor residue Arg 79 is substituted with any of a residue selected from the group Lys, His, Cys, Met, Phe, Tyr, Trp, Pro, Gly, Ala, Val, Ile, Leu, Ser, Thr, Asp, Glu, Gln, Asn, and most preferably Lys.

### Insertion of DNA into a Cloning Vehicle

The cDNA or genomic DNA is inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. Construction of suitable vectors  
5 containing the desired coding and control sequences employs standard recombinant techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated to form the desired plasmid.

Many vectors are available, and selection of the  
10 appropriate vector will depend on 1) whether it is to be used for DNA amplification or for DNA expression, 2) the size of the DNA to be inserted into the vector, and 3) the host cell to be transformed with the vector. Each vector contains various components depending on its function  
15 (amplification of DNA or expression of DNA) and the host cell for which it is compatible. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter,  
20 and a transcription termination sequence.

The preferred replicable vector is pRK5 or pRK7.

### Signal Sequence Component

In general, the signal sequence may be a component of the vector, or it may be a part of the prohormone  
25 convertase DNA that is inserted into the vector. For example the native prohormone convertase DNA encodes a signal sequence at the amino terminus (5' end of the DNA) of the polypeptide that is cleaved during post-translational processing of the polypeptide to form the  
30 mature prohormone convertase polypeptide. Included within the scope of this invention are polypeptides with the native signal sequence deleted and replaced with a heterologous signal sequence. The heterologous signal sequence selected should be one that is recognized and  
35 processed (i.e. cleaved by a signal peptidase) by the host cell. In mammalian cell expression the native signal sequence is generally satisfactory, although other mammalian signal sequences may be suitable.

### Origin of Replication Component

Most expression vectors are "shuttle" vectors, i.e. they are capable of replication in at least one class of organisms but can be transfected into another organism for  
5 expression. For example, a vector is cloned in *E. coli* and then the same vector is transfected into yeast or mammalian cells for expression even though it is not capable of replicating independently of the host cell chromosome.

DNA may also be amplified by insertion into the host  
10 genome. This is readily accomplished using *Bacillus* species as hosts, for example, by including in the vector a DNA sequence that is complementary to a sequence found in *Bacillus* genomic DNA. Transfection of *Bacillus* with this vector results in homologous recombination with the genome  
15 and insertion of the prohormone convertase subunit DNA.

### Selection Gene Component

Expression and cloning vectors should contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of  
20 transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g. ampicillin,  
25 neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media.

One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are  
30 successfully transformed with a heterologous gene express a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin (Southern et al., J. Molec. Appl. Genet., 1: 327 [1982]), mycophenolic acid (Mulligan et al.,  
35 Science, 209: 1422 [1980]) or hygromycin (Sugden et al., Mol. Cell. Biol., 5: 410-413 [1985]). The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or

neomycin (geneticin), xgpt (mycophenolic acid), or hygromycin, respectively.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the prohormone convertase nucleic acid, such as dihydrofolate reductase (DHFR) or thymidine kinase. The mammalian cell transformants are placed under selection pressure which only the transformants are uniquely adapted to survive by virtue of having taken up the marker. Selection pressure is imposed by culturing the transformants under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of both the selection gene and the DNA that encodes the polypeptide of interest. Amplification is the process by which genes in greater demand for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Increased quantities of the polypeptide of interest are synthesized from the amplified DNA.

For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity, prepared and propagated as described by Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77: 4216 [1980]. The transformed cells are then exposed to increased levels of methotrexate. This leads to the synthesis of multiple copies of the DHFR gene, and, concomitantly, multiple copies of other DNA comprising the expression vectors, such as the DNA encoding the prohormone convertase. This amplification technique can be used with any otherwise suitable host, e.g., 293 or CHO cells, ATCC No. CCL61 CHO-K1, notwithstanding the presence of endogenous DHFR if, for example, a mutant DHFR gene that is highly resistant to Mtx is employed (EP 117,060). Alternatively, host cells (particularly wild-type hosts that contain endogenous DHFR)

transformed or co-transformed with DNA sequences encoding the polypeptide of interest, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3' phosphotransferase (APH) can be selected by cell growth in  
5 medium containing a selection agent for the selectable marker such as an aminoglycosidic antibiotic, e.g., kanamycin, neomycin, or G418. See U.S. Pat. No. 4,965,199.  
**Promoter Component**

Expression and cloning vectors usually contain a  
10 promoter that is recognized by the host organism and is operably linked to the nucleic acid encoding the polypeptide of interest. Promoters are untranslated sequences located upstream (5') to the start codon of a structural gene (generally within about 100 to 1000 bp)  
15 that control the transcription and translation of a particular nucleic acid sequence, such as that encoding a prohormone convertase, to which they are operably linked. Such promoters typically fall into two classes, inducible and constitutive. Inducible promoters are promoters that  
20 initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, e.g. the presence or absence of a nutrient or a change in temperature. At this time a large number of promoters recognized by a variety of potential host cells  
25 are well known. These promoters are operably linked to DNA encoding the polypeptide of interest by removing the promoter from the source DNA by restriction enzyme digestion and inserting the isolated promoter sequence into the vector. Both the native promoter sequence and many  
30 heterologous promoters may be used to direct amplification and/or expression of the polypeptide of interest. However, heterologous promoters are preferred, as they generally permit greater transcription and higher yields of expressed polypeptide of interest as compared to the native  
35 prohormone convertase promoter.

Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found

70 to 80 bases upstream from the start of transcription of many genes is a CXCAAT region where X may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into mammalian expression vectors.

Polypeptide transcription from vectors in mammalian host cells is controlled by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g. the actin promoter or an immunoglobulin promoter, from heat-shock promoters, and from the promoter normally associated with the polypeptide of interest, provided such promoters are compatible with the host cell systems.

The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication. Fiers et al., Nature, 273:113 (1978); Mulligan and Berg, Science, 209: 1422-1427 (1980); Pavlakis et al., Proc. Natl. Acad. Sci. USA, 78: 7398-7402 (1981). The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. Greenaway et al., Gene, 18: 355-360 (1982). A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. 4,419,446. A modification of this system is described in U.S. 4,601,978. See also Gray et al., Nature, 295: 503-508 (1982) on expressing cDNA encoding immune interferon in monkey cells; , Reyes et al., Nature, 297: 598-601 (1982) on expression of human -interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus, Canaani and Berg, Proc. Natl. Acad. Sci. USA, 79: 5166-5170 (1982) on expression of the human interferon 1 gene in cultured mouse and rabbit cells, and Gorman et al., Proc.

Natl. Acad. Sci. USA, 79: 6777- 6781 (1982) on expression of bacterial CAT sequences in CV-1 monkey kidney cells, chicken embryo fibroblasts, Chinese hamster ovary cells, HeLa cells, and mouse NIH-3T3 cells using the Rous sarcoma virus long terminal repeat as a promoter.

#### Enhancer Element Component

Transcription of a DNA encoding the polypeptide of interest of this invention by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10-300 bp, that act on a promoter to increase its transcription. Enhancers are relatively orientation and position independent having been found 5' (Laimins et al., Proc. Natl. Acad. Sci. USA, 78: 993 [1981]) and 3' (Lusky et al., Mol. Cell Bio., 3: 1108 [1983]) to the transcription unit, within an intron (Banerji et al., Cell, 33: 729 [1983]) as well as within the coding sequence itself (Osborne et al., Mol. Cell Bio., 4: 1293 [1984]). Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, a-fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, Nature, 297: 17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the desired DNA, but is preferably located at a site 5' from the promoter.

#### Transcription Termination Component

Expression vectors used in eukaryotic host cells (insect, plant, animal, human, or mammalian cells) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3' untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the



mRNA encoding the prohormone convertase. The 3' untranslated regions also include transcription termination sites.

Construction of suitable vectors containing one or more of the above listed components and including the desired coding and control sequences employs standard ligation techniques. Isolated plasmids or nucleic acid fragments are cleaved, tailored, and religated in the form desired to generate the plasmids required.

Particularly useful in the practice of this invention are expression vectors that provide for the transient expression in mammalian cells of DNA encoding the polypeptide of interest. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a desired polypeptide encoded by the expression vector. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of polypeptides encoded by cloned DNAs, as well as for the rapid screening of such polypeptides for desired biological or physiological properties. Thus, transient expression systems are particularly useful in the invention for purposes of identifying polypeptide analogs and variants that have desired activity.

Other methods, vectors, and host cells suitable for adaptation to the synthesis of the prohormone convertase and other polypeptides of this invention in recombinant mammalian cell culture are described in Gething et al., Nature, 293: 620-625 [1981]; Mantei et al., Nature, 281: 40-46 [1979]; Levinson et al.; EP 117,060; and EP 117,058. A particularly useful plasmid for mammalian cell culture expression of the prohormone convertase subunit is pRK5 (EP pub. no. 307,247) or pSVI6B.

#### Selection and Transformation of Host Cells

Suitable host cells for cloning or expressing the vectors herein are the higher eukaryote cells described above. Suitable host cells for the expression of

glycosylated polypeptide are derived from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture. Examples of invertebrate cells include plant and insect cells. However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure in recent years [Tissue Culture, Academic Press, Kruse and Patterson, editors (1973)]. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36: 59 [1977]); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77: 4216 [1980]); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23: 243-251 [1980]); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL- 1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather et al., Annals N.Y. Acad. Sci., 383: 44-68 [1982]); MRC 5 cells; FS4 cells; and a human hepatoma cell line (Hep G2). Preferred host cells are human embryonic kidney 293 and Chinese hamster ovary cells.

Host cells are transfected and preferably transformed with the above-described expression or cloning vectors of this invention and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

It is further envisioned that the cells comprising nucleic acid encoding the polypeptide of interest of this invention may be produced by homologous recombination, or with recombinant production methods utilizing control

elements introduced into cells already containing nucleic acid encoding the polypeptide of interest currently in use in the field. For example, a powerful promoter/enhancer element, a suppressor, or an exogenous transcription  
5 modulatory element is inserted in the genome of the intended host cell in proximity and orientation sufficient to influence the transcription of nucleic acid encoding a desired prohormone convertase. The control element does not encode the prohormone convertase of this invention, but  
10 affects the prohormone convertase nucleic acid which is present in the host cell genome. One next screens for cells making the prohormone convertase of this invention, or increased or decreased levels of expression, as desired.

Mammalian cells may be stably transformed using any  
15 acceptable vector known to transform a particular cell type. A preferred vector is the pRK5 used in the present invention with 293 human kidney cell. For example, the mammalian cells are transformed to produce a prohormone convertase and these cells are then used to produce  
20 properly processed hormone by transforming them to express a prohormone. Among the preferred prohormones are those that when processed result in hormones containing two or more polypeptide chains. Preferred two chain hormones are relaxin and insulin.

#### 25 Culturing the host cells

Prokaryotic cells used to produce the polypeptide of this invention are cultured in suitable media as described generally in Sambrook et al., *supra*.

The mammalian host cells used to produce the  
30 polypeptides of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ([MEM], Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ([DMEM], Sigma) are suitable for culturing the host cells. In  
35 addition, any of the media described in Ham and Wallace, Meth. Enz., 58: 44 (1979), Barnes and Sato, Anal. Biochem., 102: 255 (1980), U.S. 4,767,704; 4,657,866; 4,927,762; or 4,560,655; WO 90/03430; WO 87/00195; U.S. Pat. Re. 30,985; or U.S. 5,122,469, issued 16-Jun-1992 may be used as

culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as Gentamycin<sup>TM</sup> drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

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The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. Various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The following examples are intended to illustrate the best mode now known for practicing the invention, but the invention is not to be considered limited to these examples.

#### EXAMPLE 1

##### Cloning of Murine Prohormone Convertases Type 1 (mPC1) and Type 2 (mPC2)

The mouse pituitary tumor cell line, AtT20, was used as the source for candidate prohormone convertase mRNA's. The AtT-20 cell line was obtained from the American Type Culture Collection (Rockville, MD). Cells were grown in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. Total RNA was prepared from confluent cells (Maniatis 1983) and cDNA was generated by incubation of 5ug total RNA with 400 U Moloney murine leukemia virus reverse transcriptase (GIBCO-BRL), 2.5 mg GeneAmp 10 X reaction buffer (Perkin Elmer-Cetus), 20 U RNasin

ribonuclease inhibitor (Promega), 400mM dNTPs, 0.5 mg oligo-dT (United States Biochemical), 1.4 mM MgCl<sub>2</sub>, 10 mM DTT; all in a total volume of 25 uL for 1 hour at 37 degrees C.

Amplification using a degenerate polymerase chain  
5 reaction (PCR) of candidate prohormone convertase targets  
was carried out in the same reaction tube by adding 50 pmol  
each of forward and reverse MOPAC PCR primers, 0.02 mmol  
dNTPs, with an additional 7.5 mL 10X reaction buffer plus 5  
U Taq DNA polymerase. The primer sequences were based on  
10 the conserved aspartate and serine catalytic residues of  
KEX2, PC2, Proprotease B, and subtilisin BPN as described in  
Smeekens, et al (The Journal of Biological Chemistry Vol  
265, pp. 2997-3000 [1990]). The forward primer used was:  
5'GCAAAATCTAGA(C/T)(G/T)GCIAT(C/T)GTIGA(C/T)GA(G/T)GGI3'  
15 (Seq. ID #5) and the reverse primer was:  
5'AAGCATGAGCTCIGG(A/G)GC(A/G)GC(A/G)GCIGAICC3' (Seq. ID #6).  
Thirty cycles of degenerate PCR were done, each consisting  
of denaturation (1 min, 94 degrees C), primer annealing (2  
min, 48 degrees C for the first 5 cycles; 2 min at 55  
20 degrees C thereafter), and primer extension (3 min, 72  
degrees C). The products from the PCR reaction were  
electrophoresed in a 2.5% NuSieve-GTG low melting agarose  
gel (FMC). Discrete bands of approximately 600 bp were  
excised and subcloned into pUC118 for DNA sequence analysis.  
25 Partial mPC1 and mPC2 sequences were derived by this  
procedure.

A cDNA pool was prepared as a source of template for  
the cloning of full length sequences of the candidate PC  
enzymes (Frohman 1988; Innis 1990). Mouse AtT-20 total RNA  
30 (5mg) was heated for 3 min at 65°C and immediately chilled  
on ice. The denatured RNA was added together with 200 U  
reverse transcriptase to a first strand cDNA synthesis  
reaction containing 4 mL 5 X H-RT buffer (GIBCO-BRL), 10 mM  
DTT, 1 mM dNTPs, 20 U RNasin, and 2.5 pmol R<sub>0</sub>R<sub>1</sub>-d(T)<sub>17</sub>  
35 adapter primer: 5' GATATCACTCAGATCGATGAATTCGAGCTC(T)<sub>17</sub> 3'  
(Seq. ID #7) all in a final volume of 20uL. The mixture was  
incubated for 1 hour at 37 degrees C and diluted to 1 mL  
with Tris/EDTA. Aliquots (5-10 uL) of the cDNA pool were  
used for amplifications of unknown 3' and 5' regions by

RACE-PCR (rapid amplification of cDNA ends, Frohman 1988; Innis 1990) using a combination of gene-specific PCR primers (for mPC1 they were: 3'RACE primer 5'AAGCTTTCTAGAGGATCCCTCTGGTGGATTGG3' (Seq ID #8) and 5'RACE primer 5'AAGCTTGAATTCTCCAACCCACACTTGTG3' (Seq. ID #9) and the inner adapter R<sub>i</sub> PCR primer 5' AGATCGATGAATTCGAGCTC 3' (Seq. ID No. 10). Final construction of the full length mPC1 and mPC2 cDNAs was through the technique of recombinant PCR (Innis 1990). All PCR cloning reactions were carried out with Vent DNA polymerase (New England Biolabs) to minimize the introduction of mismatched bases during amplification of template.

All mPC clones were sequenced with the Sequenase 2.0 kit from USB and cloned into PUC118 (Vieira, et al Methods Enzymology 153 [1987]).

## EXAMPLE 2

### Relaxin Production in Transfected Cells

#### Construction of relaxin and prohormone convertase expression vectors

The cDNA clone of the preprorelaxin gene, pCIS.Rx, provided the coding sequence of the human preprorelaxin. The pCIS mammalian expression vector is described in (Gorman DNA Prot Eng Tech 2:3-10, 1990). The cDNA encoding H2 preprorelaxin was excised from the cloning vector as described in Hudson, P et al., The EMBO Journal 3, 2333-2339, [1984] by using a complete Hpa II digest followed by a Hinf I partial digest. pCIS.Rx was digested by restriction endonucleases XBA I and ECO RI to excise the coding region of preprorelaxin. pRK7 was digested by restriction endonucleases XBA I and ECO RI. The resultant XBA I/ECO RI human preprorelaxin coding region was ligated into the XBA I/ECO RI digested pRK7 yielding the final preprorelaxin mammalian expression vector, pRK.Rx.

The cDNA clone of the mPC1 gene, PUC118.mPC1 from example 1, provided the coding sequence of the mPC1 for construction of plasmids to direct the expression of mPC1 in transfected mammalian cells. PUC118.mPC1 is digested with restriction endonucleases SAC I and ECO RI. pRK7 is

digested with restriction endonucleases SAC I and ECO RI. The resultant SAC I/ECO RI mPC1 coding region is ligated into the SAC I/ECO RI digested pRK7 to yield the final mPC1 mammalian expression vector, pRK.mPC1.

5       The cDNA clone of the mPC2 gene, PUC118.mPC2 from example 1, provided the coding sequence of the mPC2 for construction of plasmids to direct the expression of mPC2 in transfected mammalian cells. PUC118.mPC2 is digested with restriction endonucleases XBA I and ECO RI. pRK7 is  
10       digested with restriction endonuclease XBA I and ECO RI. The resultant XBA I/ECO RI mPC2 coding region is ligated into the XBA I/ECO RI digested pRK7 to yield the final mPC2 mammalian expression vector, pRK.mPC2.

      The cDNA clone of the KEX2 gene, pYEp24.pJ28 (Julius, et al, Cell vol 37, p 1075 [1984]), provided the coding  
15       sequence of the KEX2 gene for construction of the final KEX2 mammalian expression plasmid. Vector pYEp24.pJ28 was digested with restriction endonuclease Eco RI and run on an Agarose gel. A 3.3 kb fragment containing the coding  
20       region was isolated. pRK5 was digested with restriction endonuclease Eco RI, and then treated with bacterial alkaline phosphatase (BAP). The Eco RI digested, BAP treated pRK5 was run on an agarose gel and a 4.7 kb fragment was isolated.

25       The 3.3 kb fragment of pYEp24.pJ28 was ligated to the 4.7kb fragment of pRK5 to form vector pRK.KEX.RI. pRK.KEX.RI was digested with restriction nuclease Dde I, then treated with Klenow, and further digested with restriction endonuclease Hind III. The Dde I/Hind III  
30       treated pRK.KEX.RI was run on a polyacrylamide gel and a 425bp fragment was isolated. pRK5 was digested with restriction endonuclease Sma I/Hind III, then treated with BAP, run on an agarose gel and a 4.7kb fragment was isolated. The 4.7kb fragment of pRK5 was ligated to the  
35       425 bp fragment of pRK.KEX.RI to form vector pRK5.5'KEX. pRK5.5'KEX was digested with Hind III and treated with BAP. A 2 kb Hind III fragment encoding the 3' end of KEX2 was derived from vector pYEp24.pJ28 and was ligated to the Hind III/BAP treated vector pRK5.5'.KEX forming the final KEX

mammalian expression vector pRK.KEX2 which directs the expression of KEX2 in transfected mammalian cells.

Transient transfection of relaxin in human kidney 293 cells.

5 Human Kidney 293 cells were subjected to transient transfection by the method of Gorman (Gorman DNA Prot Eng Tech 2:3-10, 1990). Expression vector containing prorelaxin cDNA, pRK.Rx, (10ug) was transfected into 293 cells alone (100 mm dish), or together with an equal amount  
10 of expression vectors for mPC1 (pRK.mPC1), mPC2 (pRK.mPC2) or kex2 (pRK.kex2) cDNAs.

Stable transfection of relaxin in Human Kidney 293 Cells

15 General aspects of mammalian cell host system transformations have been described by Axel in U.S. 4,399,216 issued 16 August 1983. The preferred method for stable transformation of a mammalian cell of the present invention is the calcium phosphate precipitation method described in sections 16.30-16.37 of Sambrook et al, *supra*.  
20 The preferred host cell is the human embryonic kidney line (293 ) or Chinese hamster ovary cells/-DHFR(CHO). The preferred media contains the antibiotic neomycin or geneticin.

Characterization of Processed Relaxin

25 Immunoaffinity purification

Following transfection, culture medium was removed and replaced by 2mL DMEM (minus cysteine and methionine) containing 200uCi each of 35S-cysteine and 35S-methionine (Amersham). After a 3 hr incubation, the supernatant was  
30 collected and cells were washed with PBS. Cells were lysed with 1 mL lysis buffer (150 mM NaCl, 1% NP-40, 50mM Tris-HCl pH 8.0). Both supernatant and whole-cell lysate were analyzed by immunoprecipitation.

Supernatants (500uL) and whole-cell lysates (250uL)  
35 from the transfections were mixed with 5 mg of anti-relaxin monoclonal antibody (MAbRlx6) for an overnight incubation, with gentle rocking at 4 degrees C. Antibody-antigen complexes were absorbed onto protein A-Sepharose CL4B beads (Pharmacia-LKB) at 4 degrees C for 1 hour. The beads were



briefly centrifuged and gently washed three times with lysis buffer. Liquid was aspirated off and 50 mL 2 X tricine/SDS sample buffer (25% glycerol, 8% SDS, 1.5% Serva Blue G, 0.9 M Tris-HCl pH 8.45) was added to the beads.

- 5 Samples were heated for 10 min at 85 degrees C and 10uL aliquots were applied to pre-cast tricine/SDS 10-20% polyacrylamide gradient gels (Novex). Following electrophoresis, gels were fixed, soaked in Ampligy (Amersham), dried and exposed to X-ray film at -80 degree
- 10 C.

Following transfection of 293 cells with the expression plasmid for prorelaxin, pRK.Rx, only the precursor prorelaxin immunoprecipitated from cell lysates or cell supernatants. The prorelaxin bands at about 6.0 KD

15 on a 10-20% polyacrylamide gradient gel.

Co-transfection of 293 cells with the expression plasmid for prorelaxin, pRK.Rx, and pRK.mPC2, which directs expression of the mouse mPC2 cDNA, yields only the precursor prorelaxin, indicating that mPC2 is not involved

20 in processing native prorelaxin in this system.

Co-expression of prorelaxin and mPC1 cDNA's or prorelaxin and KEX2 yielded mature, bonafide relaxin, which bands at about 3.0 KD on a 10-20% polyacrylamide gradient gel.

25 **Reverse phase HPLC and mass spectrometry analysis**

For preparative analysis of cell-secreted protein, three 10 cm dishes of confluent cells were transfected with substrate proH2Relaxin alone, or with a combination of proH2Relaxin (wild-type or mutant) and processing enzyme

30 cDNAs. A total of 30 uL of supernatant was collected from each transfection and passed twice over a small (300uL) column of anti-relaxin monoclonal antibody linked to Sepharose-CL4B for immunoaffinity purification. The column was washed with PBS and non-specifically absorbed material

35 was removed by a 1 M NaCl in PBS wash, followed by 2 M guanidine-HCl in 10 mM Tris-HCl pH 7.5. Antibody-bound protein was eluted with a small volume of 4 M guanidine-HCl/Tris-HCl.

The immunoaffinity column eluant was applied without further purification to a 2 X 100 mm RP-C<sub>4</sub> reverse phase HPLC column (Synchrom). Material was eluted by application of a linear gradient of acetonitrile in 0.1% Trifluoroacetic acid from 20% (0-5 min) to 60% (5-45 min). The flow rate was held at 0.5 mL/min and the absorbance at the column outlet was monitored at 214 nm. Eluants from major peaks of absorbance were collected for analysis by mass spectrometry (Figure 8).

The intact molecular weights of prorelaxin and processed relaxin were measured by electrospray ionization mass spectrometry. Micromolar solutions (1-10pmol/ul) of protein in aqueous acetonitrile (50/50, v/v) with 1% acetic acid were infused at 1.5 ul/min into a SCIEX API III mass spectrometer. The quadrupole mass spectrometer was operated with the Ionspray articulated nebulizer (SCIEX, Thornhill, Canada) at 4600 V, the interface plate at 600 V, and the orifice at 100-120V.

Data were collected every 0.1 v with the quadrupole scanning from 600-2200 u in 32 seconds. Molecular weights of the individual A and B chains were determined by fast atom bombardment (FAB) mass spectrometry following on-probe reduction as described by Stults et al. (Biomed Environ Mass Spectrom 19:655-664 (1991)).

Transfection of PRK.Rx alone resulted in the secretion of prorelaxin as the major product. This species had an HPLC elution time of 29 minutes. Co-transfection of PRK.Rx with either PRK.mPC1 or PRK.KEX2 generated a major species that gave an HPLC retention time of 17 minutes. This retention time was very similar to that observed for authentic mature relaxin purified from human corpus luteum.

Co-transfection major peaks eluting from the column were collected for analysis by mass spectrometry. Electrospray measurements generated mass values consistent with authentic mature relaxin. This was confirmed further by fast atom bombardment analysis of reduced 5963 Da species. Two peaks of 2657 and 3313 mass units were obtained, exactly corresponding to the predicted values for reduced relaxin A and B chains, respectively. Material

from the 5963 Da relaxin was subjected to several rounds of N-terminal peptide sequencing in a gas phase sequencer. No sequence was obtained for the A-chain as expected due to the pyroglutamyl residue that blocks its N-terminus. All amino acids detected were from the B chain and had a peptide sequence consistent with correct removal of the 24 amino acid signal sequence that precedes the B chain. Additionally, the mature B-chain terminates with a serine residue at its C-terminus suggesting that carboxypeptidase activity present in the 293 cells removed the residual basic residues, KR, which remain following cleavage at the B-chain / C-peptide junction.

### EXAMPLE 3

#### Human Relaxin Mutants and PC Specificity

Prohormone convertase substrate specificity is exemplified by processing of human prorelaxin mutants. A series of mutant prorelaxin cDNAs were made in which basic residues thought to be required for processing were replaced with alanine. Two dibasic residues, KR, are located at the B-chain / C-peptide junction and both are required for processing. When either of these basic amino acids is replaced by alanine, unprocessed prorelaxin is secreted from the 293 cells. There is no indication of intermediate proteins indicative of a partially processed precursor, which might have resulted from partial cleavage at the C-peptide / A-chain junction.

#### Site-directed mutagenesis of prorelaxin

Site-directed mutagenesis was performed on the relaxin mammalian expression vector, pRK.Rx, by the method of Kunkel (Kunkel 1987), with some minor modifications. Transformation-competent (CaCl<sub>2</sub>) CJ236 strain of *E. Coli* was used as the bacterial host for the synthesis of uracil-containing template phagemid DNA, and T<sub>4</sub> enzyme. The oligonucleotide extension reaction was performed in a 10 uL volume for an initial period of 15 min at room temperature, followed by a 75 min incubation at 37 degrees C. The reaction was terminated by the addition of Tris/EDTA buffer to a final volume of 50 uL. A 10 uL aliquot was used to transform an *ung*<sup>+</sup> strain of *E. coli*, MM299, for selection

against uracil-containing wild-type template DNA. This strain was also used to produce single strand DNA for use in sequencing analysis by the chain termination method (Sequenase kit, United States Biochemical).

### 5 Identification of prohormone convertase substrate specificity.

Prorelaxin alanine mutations of the basic residues K and R were constructed to define murine prohormone convertase 1 specificity. Figure 11. The following  
10 mutations were tested for substrate specificity to murine prohormone convertase 1: 1.4, 2.4, 3.2, 4.3, 7.2 and 8.6. The relaxin (Rx) mutants have the following sequence in the prohormone convertase cleavage site.

### 15 C-chain/A-chain junction mutants

	Native Rx	H S R K K R Q (Seq. No. #48)
		CAT TCT CGA AAA AAG AGA CAA (Seq. No. #11)
20	Rx 1.4	H S V K K R Q (Seq. No. #49)
		CAT TCT GTA AAA AAG AGA CAA (Seq. No. #12)
	Rx 2.4	H S R A K R Q (Seq. No. #50)
		CAT TCT AGA GCA AAG AGA CAA (Seq. No. #13)
25	Rx 3.2	H S R K A R Q (Seq. No. #51)
		CAT TCT AGA AAA GCA AGA CAA (Seq. No. #14)
	Rx 4.3	H S R K R A Q (Seq. No. #52)
30		CAT TCT AGA AAA AGA GCA CAA (Seq. No. #15)

### B-chain/C-chain junction mutants

	Native Rx	T W S K R S L (Seq. No. #53)
35		ACC TGG AGC AAA AGG TCT CTG (Seq. No. #16)
	Rx7.2	T W S A R S L (Seq. No. #54)
		ACC TGG AGC GCT AGG TCT CTG (Seq. No. #17)

Rx8.6

T W S K A S L (Seq. No. #55)

ACC TGG AGC AAA GGT TCT CTG (Seq. No. #18)

Figure 9 illustrates murine prohormone convertase 1 processing of these mutants. Mutants 1.4 and 2.4 are processed the same as wild-type and mutant 3.2 is partially processed. Mutant 4.3 doesn't appear to be processed and mutants 7.2 and 8.6 are not processed. Disrupting the B-C chain junction at either the position mutated at mutants 7.2 or 8.6 prevents any cleavage of prorelaxin. The C-A chain is probably not available for cleavage by murine prohormone convertase 1 until the B-C chain junction is cleaved. This data supports a progressive cleavage mechanism involving cleavage of this upstream site first. The B-C chain site requires both basic residues. Mutants 3.2 and 4.3 point out that while basic residues are required (as seen with 7.2 and 8.6) they are not sufficient. Both mutants 3.2 and 4.3 have intact KR sites and mutant 3.2 is not cleaved as well as wild-type and mutant 4.3 is not cleaved by murine prohormone convertase 1.

Murine prohormone convertase 2 does not cleave the wildtype prorelaxin. Murine prohormone convertase 2 does not cleave any of the prorelaxin mutants with the exception of 4.3 where there is some processing. This suggests that there is a difference in the specificity of cleavage for murine prohormone convertase 1 and murine prohormone convertase 2 which is defined by sequences other than the dibasic residues. Non-substrate proteins can be made to be substrates by appropriate mutagenesis. Mutant 7.2 is not cleaved by murine prohormone convertase 2. Mutation of an upstream site in prorelaxin prevents downstream cleavage illustrating the presence of progressive cleavage of prorelaxin.

#### EXAMPLE 4

##### Construction of Proinsulin Mutants and Insulin Expression in Transfected 293 Cells

The cDNA clone of the human preproinsulin gene, pSVEHIGDHFR, described in Australian patent 616,201 issued

February 18, 1992, provided the coding sequence of the human preproinsulin gene for the final mammalian expression vector. Aliquots (5-10 uL) of pSVEHIGDHFR were used for amplification of the coding region by RACE-PCR (rapid  
 5 amplification of cDNA ends, Frohman 1988; Innis 1990) using a combination of gene-specific PCR primers: for the 5' end they were CAT AAG CTT ACC ATG GCC CTG TGG ATG CGC (Seq ID #18) (sequence given 5' to 3') and for the 3' end they were  
 10 CAT TCT AGA CTA GTT GCA GTA GTT CTC CAG (Seq. ID #19) (sequence given 5' to 3'). All PCR cloning reactions were carried out with Vent DNA polymerase (New England Biolabs) to minimize the introduction of mismatched bases during amplification of template. All proinsulin clones were sequenced with the Sequenase 2.0 kit from USB and cloned  
 15 into restriction digested pRK5. The final preproinsulin mammalian vector is pRK.proins.

A human proinsulin mutant having a non-naturally occurring prohormone convertase cleavage site is constructed by mutating the human proinsulin cDNA,  
 20 pRK.proins, encoding the naturally occurring basic cleavage site at the B-chain/C-peptide junction (KTRR) (Seq ID #20) and/or A-chain/C-peptide junction (LQKR) (Seq ID #21) by site-directed mutagenesis (Kunkel 1987). The following proinsulin variants were constructed: proins.RTKR.Ip (Seq  
 25 ID #22), proins.RQKR.IIp (Seq ID #23), proins.KTKR.Ip (Seq ID #24). The following double proinsulin variants were constructed: proins.KR.Ip/RQKR.IIp (Seq ID #23), and proins.RTKR.Ip (Seq. ID #22)/RQKR.IIp (Seq. ID #23). Ip is the Type I enzyme cleavage site and IIp is the Type II  
 30 enzyme cleavage site.

Primers used in proinsulin mutant construction were the following:

35	PROINS.RTKR.Ip	CTCTGCCTCCCGCTTGGTCTCGGTGTGTAG (Seq. ID #25)
	PROINS.RQKR.IIp	CACGCTTCTGCCGGGATCCCTC (Seq. ID #26)
	PROINS.KTKR.Ip	CTCTGCCTCCCGCTTGGTCTCGGTGTGTAG (Seq. ID #27)

The sequences are listed in 5'-->3' orientation.

The double proinsulin mutant proins.KR.Ip/RQKR.IIp (Seq. ID #23) changes the native human proinsulin residue  
5 Arg 31 to Lys 31 at the Type I enzyme cleavage site, and  
proinsulin residue Leu 62 is changed to Arg 62 at the Type  
II enzyme cleavage site.

The double proinsulin mutant proins RTKR.Ip (Seq. ID  
#22)/RQKR.IIp (Seq. ID #23) changes the native human  
10 proinsulin residue Lys 29 to Arg 29 at the Type I enzyme  
cleavage site, residue Arg 31 to Lys 31 at the Type I  
enzyme cleavage site and proinsulin residue Leu 62 is  
changed to Arg 62 at the Type II enzyme cleavage site.

All mutants were screened through the primer regions  
15 with the Sequenase 2.0 kit from USB.

DNA from all proinsulin mutants and naturally  
occurring proinsulin was CsCl banded and used for 293 cell  
transient transfection by the method of Gorman (Gorman DNA  
Prot Eng Tech 2:3-10, 1990). The next day, cells were  
20 labeled with <sup>35</sup>S Met and <sup>35</sup>S Cys (200uCi/ml) and labeled for  
4-6 hours.

#### Immunoaffinity purification

Supernatants (500uL) or whole-cell lysates (500uL)  
from the transfections were mixed with 4 ul of Conc. Guinea  
25 Pig Anti-Human Insulin Lot I01, from Biomedica for an  
overnight incubation, with gentle rocking at 4 degrees C.  
Protein A Sepharose (CL4B-Pharmacia 17-0963-03) was  
prepared by washing 5 mls of Protein A Sepharose with NP40  
lysis buffer. The wash procedure was repeated 4 times.  
30 After the last wash was aspirated, enough buffer was added  
to provide a 25% v/v slurry of Protein A Sepharose-CL4B.

100 ul 25% protein A slurry was added to each overnight  
sample containing the Conc. Guinea Pig Anti-Human Insulin  
Lot I01, from Biomedica. Incubate 1 hour at 4 degrees with  
35 rocking. Centrifuge 15 seconds, aspirate supernatant into  
waste, and wash 3 times with NP 40 lysis buffer. Aspirate  
buffer. Add 30 ul 2x Tricine-SDS sample buffer to each  
sample tube. Heat 100 degrees for 10 minutes and apply  
10uL aliquots to pre-cast tricine/SDS 16% polyacrylamide

gradient gels (Novex). Following electrophoresis, gels were fixed, soaked in Ampligy (Amersham), dried and exposed to X-ray film at -80 degree C.

#### Gel results

5 Transfections using native human proinsulin DNA resulted in a prominent protein band at 6.5 KD and a faint band at 3.4 KD. Transfections using the DNA of proinsulin variant proins.RTKR.Ip (Seq. ID #22)/RQKR.IIp (Seq. ID #23), resulted in protein bands at 3.4KD and 2.35  
10 KD where authentic insulin B and A chains, respectively, run on 16% tricine/SDS polyacrylamide gradient gels (NOVEX).

Transfections using the DNA of proinsulin mutants, proins.RQKR.IIp (Seq. ID #23) or double mutant  
15 proins.KR.Ip/RQKR.IIp (Seq. ID #23), resulted in two bands, one band at about 6.0 KD representing the B-chain/C-peptide intermediate band and one band at 2.35 KD representing the insulin A-chain.

Transfections using the DNA of proinsulin variant, proins.RTKR.Ip (Seq. ID #22), resulted in two bands, one  
20 band running slightly below the B-chain/C-peptide intermediate band representing the C-peptide/A-chain intermediate band and one band at 3.4 KD representing the insulin B-chain.

25 Transfections using the DNA of proinsulin mutant, proins.KTKR.Ip (Seq. ID #24) resulted in one prominent band at 6.5 KD and a faint band at 3.4 KD.

#### EXAMPLE 5

##### Construction of Prohormone Convertase Mutants

30 Prohormone convertase precursor residues involved in processing of the precursor form of the prohormone convertase to the bioactive form of the prohormone convertase are mutated such that the prohormone convertase precursor is processed by the prohormone convertase  
35 naturally occurring in the human kidney 293 cell

Site-directed mutagenesis of the mammalian expression vector, pRK.mPC1 or mammalian expression vector, pRK.mPC2 is by the method of Kunkel (Kunkel 1987). The following



primers were used in the Prohormone Convertase precursor mutant construction:

mPC1 primer GAT ATG AAG AGC AGA TCT TTT GGA CCT CCG AGG ATG  
5 (Seq. ID #28)

mPC2 primer CTT ATG GTG TAA GCT TCG TTT TGC TCT GGC CTT TGC  
AAG (Seq. ID #29)

10 where primers are given in a 5' to 3' direction.

The PC1 primer results in a mammalian prohormone convertase 1 mutant having the native residue ARG.80 mutated to LYS.80.

The PC2 primer results in a prohormone convertase  
15 mutant having the native mammalian prohormone convertase 2 residues LYS.77 ARG.78 ARG.79 mutated to ARG.77 ALA.78 LYS.79

All mutants were screened through the primer regions with the Sequenase 2.0 kit from USB.

#### EXAMPLE 6

20 Processing of NGF, BDNF and NT-3 Mutants by mPC 1  
and 2

To elucidate the role of the precursor in the processing of the neurotrophic factors, chimeric pRK5  
25 expression vectors were constructed to contain the precursor of NGF, NT-3, or BDNF linked to the mature portion of NGF or the NT-3 precursor linked to the mature portion of BDNF. The entire PCR amplified region of each chimera containing the NGF mature sequence was found to be  
30 identical to the published sequences for each precursor portion and for the mature NGF with the exception of a silent point mutation in codon #403 in pRK5.BDNFNGF. Plasmid vector pRK5 was used in all constructions.

Nerve Growth Factor (NGF), Neurotrophic Factor 3  
35 (NT-3), or Brain Derived Neurotrophic Factor (BDNF)

Nerve Growth Factor (NGF), Neurotrophic Factor 3 (NT-3), or Brain Derived Neurotrophic Factor (BDNF) cDNA were inserted into the cloning linker of pRK5 producing

pRK5.NGF, pRK5.BDNF, and pRK5.NT-3. Plasmid DNA was transformed into *E. coli* 294 cells and cultured to saturation in 1 liter of Super Broth (12% tryptone in H<sub>2</sub>O, 24% yeast extract in H<sub>2</sub>O, 0.5% glycerol, 70 mM K<sub>2</sub>HPO<sub>4</sub>, 25 mM KH<sub>2</sub>PO<sub>4</sub>). The plasmid DNA was isolated by alkaline lysis and purified via cesium chloride double banding according to the procedures in Sambrook et al. (1989).

#### pRK.NT3NGF plasmid construction

DNA encoding prepro NT-3 was spliced to the DNA encoding the mature portion of NGF using a polymerase chain reaction (PCR) (Saiki et al., 1985, Mullis et al. 1986). 0.5 µg of both pRK5.NT3 and pRK5.NGF were linearized with *Hind* III. The precursor portion of NT3 was amplified using primers a and b while the mature portion of NGF was amplified using the c and d primers as shown in Table 1.

PRIMER	SEQUENCE 5'-->3'	LOCATION /strand
20	a	TACAACTCACC GCGGGTCCTG (Seq ID #30) 1247-1267 NT3 /S
25	b	AAGATGGGATGGGATGATGACCGTTTCCGCCTTGATGT (Seq ID #31) 1349-1366 NT3 /AS 1407-1426 NGF /AS
30	c	ACATCACGGCGGAAACGGTCATCATCCCATCCCATCTT (Seq ID #32) 1349-1366 NT3 /S 1407-1426 NGF /S
35	d	GATATAAGCTTGAGAGTGTAGAAGGGGC (Seq ID #33) 1794-1810 NGF /AS

The location of priming within each plasmid is listed as well as the strandedness ("S" indicates sense primers and "AS" indicates antisense primers).

PCR was performed on a Thermal Cycler 460 (Perkin-Elmer Cetus) under the following conditions: 100 µL reaction volumes, 50 pmol primers, 200 µM dNTP's, 10 mM β-mercaptoethanol, 16.6 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 67 mM Tris-HCl pH 8.8, 6.7 mM MgCl<sub>2</sub>, 6.7 mM EDTA, and 0.15 mg/ml BSA. The

reaction cycle consisted of denaturation at 94 degrees C for 1 min, annealing at 55 degrees C for 1 min, and elongation at 72 degrees C for 3 min. After 35 cycles, aliquots of PCR reactions 1 and 2 were purified on an 8% acrylamide gel. Bands of 119 base pairs for the NT3 precursor and 414 base pairs for NGF mature were cut out and the DNA was recovered via electroelution as previously described (Maniatis et al. 1982).

Purified products from reactions 1 and 2 were spliced together in PCR reaction 3 using the a and d primers under the same amplification conditions. (Both a and d primers contain a restriction site that will be used for cloning back into the pRK vector.)

Final PCR reaction products were phenol/chloroform extracted, ethanol precipitated, and digested to completion with *Sst* II and *Hind* III. Digestion products were electrophoresed on a 1% NuSieve gel. The 533 base pair fragment was cut out of the gel and used in the ligation reactions described below to generate the pRK5.NT3NGF fusion plasmid.

Plasmid pRK5.NT3 was digested to completion with *Hind*III and *Eco* RI in one reaction and *Eco* RI and *Sst* II in a second reaction. Reaction products were electrophoresed on a 1% NuSieve gel. The 4681 and 337 base pair bands were cut out of the gel, melted, and ligated together with the melted 533 base pair fusion product described above according to standard protocol. (Maniatis, 1989).. Ligation products were melted for 5 minutes at 65 degrees C, diluted with 100  $\mu$ l 10 mM  $MgCl_2$ , and transformed into *E. coli* 299 cells. After picking colonies and screening them via restriction endonuclease digestion, single stranded DNA was prepared and sequenced through the entire PCR fusion area as previously stated.

#### pRK5.BDNFNGF plasmid construction

The BDNF precursor was fused to mature NGF in a similar manner as above with the exception that the fusion area was created in just one PCR reaction. 0.5 mg of *Hind* III linearized pRK5.BDNF and pRK5.NGF DNA was amplified in one reaction containing all four primers: a,b,c, and d

(Table 2). All other conditions of the amplification were as stated above. The PCR products were phenol/chloroform extracted, ethanol precipitated and digested to completion with *Bst* BI and *Hind* III. Digestion products were electrophoresed on a 1% NuSieve gel and the 650 base pair fusion band was cut out and saved for the ligation below.

Primers used in pRK5.BDNFNGF construction are shown below:

PRIMER	SEQUENCE 5'-->3'	LOCATION /STRAND
a	GGCTTGACATCATTGGCTGACACTTTCGAACACATGATAG (Seq ID #34)	1332-1371 BDNF / S
b	AAGATGGGATGGGATGATGAGCGCCGGACCCTCATGGACAT (Seq ID #35)	1533-1553 BDNF / AS 1407-1426 NGF / AS
c	ATGTCCATGAGGGTCCGGCGCTCATCATCCCATCCCATCTT (Seq ID #36)	1533-1553 BDNF / S 1407-1533 NGF / S
d	GATATAAGCTTGAGAGTGTAGAAGGGGC (Seq ID #37)	1794-1810 NGF / AS

The location of priming within each plasmid is listed as well as the strandedness ("S" indicates sense primers and "AS" indicates antisense primers).

Plasmid pRK5.BDNFNGF was constructed by digesting pRK5.BDNF to completion with *Hind* III and *Bst* BI. The products were electrophoresed on a 1% NuSieve gel. The 5181 base pair band was cut out, melted, and ligated to the melted 650 bp PCR fusion band. Ligation products were transformed, screened, and sequenced through the PCR region as stated above.

DNA for all of the above constructs was prepared via cesium chloride banding as stated earlier.

#### pRK5.NT3BDNF Plasmid Construction

Plasmid pRK5.NT-3 and pRK5.BDNF were digested to completion with *Esp* I and *Kpn* I. Digestion products were electrophoresed on a 1% NuSieve gel. The 4810 and 944 base pair fragments were cut out of the gel and ligated together. The missing 126 base pair region containing the

3' end of the NT-3 precursor and the 5' end of the BDNF mature was prepared using synthetic DNA oligonucleotides. Six overlapping primers (sense and anti-sense, Table 3) were ligated together in one reaction according to standard protocol. The ligation products were then digested with *Esp* I to generate the 126 base pair fusion fragment. Plasmid pRK5.NTBD was digested to completion with *Esp* I and ligated to the 126 base pair fragment. Following screening, pRK5.NT3BDNF was sequenced throughout the entire 126 basepair fusion area.

Primers Used in NT3BDNF Synthetic Fusion Area are shown below.

Primer      Sequence 5'-->3'

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15    1s    TGAGCGACAGCACCCCTTGGAGCCCCCGCCCTTGTATCTCATGGAGGATT  
           (Seq ID #38)

      1a    TCAGCTCCCCTCGTCGGGCGGGGTCCGAGTGCCGTTTCCGCCGTGATGTTC  
           (Seq ID #39)

      2s    ACGTGGGCAGCCCCGTGGTGGCGAACAGAACATCACGGCGGAAACGGC (Seq  
 20           ID #40)

      2a    TGTTCGCCACCACGGGGCTGCCCACGTAATCCTCCATGAGATACAAGG (Seq  
           ID #41)

      3s    ACTCGGACCCCGCCCCGACGAGGGGAGC (Seq ID #42)

      3a    GCGGGGGCTCCAAGGGGGTGCTGTCGC (Seq ID #43)

25    The "s" following the number of the plasmid indicates a sense strand plasmid and the "a" indicates an anti-sense strand. The primers were constructed to overlap each other when ligated together.

### 30    Kunkel mutagenesis

      To control for variation in the 5' portion of each gene within the vector and to optimize conditions for translation of the neurotrophic mRNA's, an 'ACC' translation consensus sequence was added to the 5' ends of  
 35    the cDNA inserts and extra base pairs of 5' sequence

originally cloned into pRK5.BDNF (including two ATG sites) and pRK5.NGF was removed. Kunkel Mutagenesis was performed on plasmids pRK5.NGF, pRK5.NT-3, pRK5.BDNF, pRK5.NT3NGF and pRK5.BDNFNGF. 2 µg plasmid DNA was transformed into CaCl<sub>2</sub> competent *E. coli* strain CJ236. Single stranded uracil containing template DNA was prepared according to Sambrook et al. (1989) with the exception that after PEG precipitation, the pellet was resuspended in 100 µL TE, extracted once with 50 µL phenol/chloroform (1:1), and twice with 500 µL chloroform. After ethanol precipitation, the pellet was resuspended in 45 µL dH<sub>2</sub>O and spun-dialysed through a Sepharose CL-6B (Pharmacia / LKB) column. 100 pmol synthetic oligonucleotide primers containing the 5' ACC (Table 4) were phosphorylated with T4 polynucleotide kinase. Mutagenesis was performed using the Muta-Gene Phagemid in vitro Mutagenesis kit (BioRad) according to manufacturer's instructions. The products were transformed into *E. coli* 299 cells and resulting colonies were picked and screened. Single stranded DNA was prepared for sequencing (Sambrook et al., 1989) with the following modifications: precipitation of the phagemid particles was at 4 degrees C followed by resuspension in 0.3 M NaOAc/1mM EDTA. DNA was extracted with a 2X volume of phenol/chloroform. The final pellet was resuspended in 50 µL dH<sub>2</sub>O. Single-stranded plasmid DNA was sequenced through the priming area with the Sequenase Version 2.0 Sequencing Kit (USB) according to manufacturer's instructions.

Table 4: Primers (antisense) used in 5' Kunkel Mutagenesis

Primer	Sequence 5'-->3'
NGF5'	GTAGAACAACATGGACATGGTGGCAATATTGTCGACTCTGGAGTCGACCTGCAG (Seq ID #44)
NT3.5'	CACATAAAACAAGATGGACATGGTCTTGTTACCTGTAGGATCCCCGG (Seq ID #45)
BDNF	5'AGTAAGGAAAAGGATGGTCATGGTGGAGGTCGACAAGCTTGAGAATTCAATCG (Seq ID #46)

The altered restriction sites used for screening purposes are underlined.

#### Cell Culture--ELISA

5 Plasmids were prepared for transfection via cesium chloride double banding.. Both the original plasmids and the 5' end mutagenized plasmids pRK5.NGF, pRK5.NT3NGF, and pRK5.BDNFNGF were transfected along with an hGH control plasmid into the human kidney cell line (293) using the  
10 calcium phosphate precipitation method (Gorman et al. 1990). 36 hours post-transfection the supernatants were assayed for NGF and hGH (as a control) expression with the enzyme linked immunosorbant assay (ELISA). ELISA's were performed by Immunoassay Services, Genentech, Inc.  
15 Supernatants of all construct transfections were also assured to have bioactivity by their effects on dorsal root ganglia and sympathetic neurons.

#### Cell culture--radioactive protein labelling

Plasmids pRK5.NGF, pRK5.NT-3, pRK5.BDNF, pRK5.NT3NGF,  
20 pRK5.BDNFNGF and pRK5.NT3BDNF were transfected into the human kidney cell line (293). 24 hours post transfection, the cells were washed with PBS and labelled for 12-14 hours with [<sup>35</sup>S]-methionine and [<sup>35</sup>S]-cysteine at 200 µCi/ml in cysteine/methionine minus DMEM media. Selected plates of  
25 cells were labelled with either [<sup>35</sup>S]-cysteine alone, or [<sup>35</sup>S]-methionine alone in cysteine minus media, or methionine minus media, respectively. The radioactive supernatants were collected and either concentrated 5-10 fold in a Centricon-10 (Amicon) according to manufacturer's  
30 instructions or immunoprecipitated along with cell lysates as stated below. One-fifth of each concentrated sample was loaded on a pre-cast 16% Tris-glycine, SDS-PAGE denaturing reducing mini-protein gel (1.5 mm) and electrophoresed according to manufacturer's directions. (Novex). The gels  
35 were fixed with Amplify (Amersham) as suggested in the instructions. Fixed, dried gels were exposed to film at -70 degree C for 8 to 24 hours.

Cell lysates were collected by washing the cells with PBS and lysing with triton lysis buffer. (1% triton, 5mM

HEPES pH 7.2). Cell debris was removed by centrifugation. Lysates and supernatants were immunoprecipitated as follows.

Rabbit anti-NGF and goat anti-hGH antibodies were provided by Immunoassay Services, Genentech, Inc. One half of each supernatant and lysate was immunoprecipitated with rabbit anti-NGF antibodies alone. The other half, serving as a transfection control, was co-immunoprecipitated with the rabbit anti-NGF and goat anti-hGH antibodies.

[<sup>35</sup>S]-labelled supernatants and lysates were preincubated with 100 µL 10% Pansorbin cells (*Staphylococcus aureus*) in phosphate buffered saline (Calbiochem) for 30 to 60 minutes at 4 degrees C with rotation. Cells were removed by centrifugation and the supernatants were incubated as above with saturating levels of rabbit anti-NGF antibodies or rabbit anti-NGF and goat anti-hGH antibodies. 120 µL 10% Pansorbin cells were added to the mixture and incubated for 1 hour at 4 degrees C with rotation. Each tube was centrifuged for 2 minutes in a microcentrifuge. Supernatants were removed and the pellets were washed once with Buffer #1 (1M NaCl, 0.05 M Tris pH 6.8 in water), twice with Buffer #2 (1M Tris pH 8.8, 0.2M NaCl, 1% NP40, 0.3% SDS), and once with cold dH<sub>2</sub>O. Washed pellets were resuspended in 40 µL 2X Tris-Glycine SDS loading buffer. 20 µL was loaded on a pre-cast 16% Tris-glycine SDS reducing mini-protein gel (1.5 mm) and electrophoresed according to manufacturer's directions. (Novex). The gels were fixed with En<sup>3</sup>Hance (Dupont) as suggested with the exception that the final wash in water included 5% glycerol to avoid gel cracking.

Fixed, dried gels were exposed to film at -70 degrees C for 9-66 hours.

#### Effects of precursor on NGF expression

The effects of the 5' mutations on secreted NGF levels were determined by three hGH controlled experiments performed in duplicate. In these experiments, the hGH controlled for potential differences due to transfection efficiencies. For example, in any one experiment, NGF and



hGH expression varied with each plate. Since each NGF expression value was compared only to the hGH expression in the same plate, relative comparisons could be made.

The results of the 5' changed plasmids (pRK5.NGF 5'ACC, pRK5.NT3NGF5'ACC, and pRK5.BDNFNGF 5'ACC) are summarized in Table 5. The chimeric proteins were compared to the wildtype NGF expression level which was set at 100 %. Though there seems to be about a 2-fold difference in the levels of NGF production from pRK5.NGF and pRK5.NT3NGF, the production levels from pRK5.BDNFNGF have dropped about 50-fold.

Table 5: Effects of Precursor on Expression.

Plasmid	NGF/hGH	Average	% of NGF Expression
pRK5.NGF5'ACC	0.194 0.215 0.328 0.286 0.266 0.264	0.258	100
pRK5.NT3NGF5'ACC	0.105 0.169 0.163 0.149 0.148	0.147	57
pRK5.BDNFNGF5'ACC	0.007 0.007 0.006 0.006 0.005 0.004	0.006	2

Since it is in its normal form (wildtype), pRK5.NGF5'ACC was given the value of 100 %. The two chimeras were then compared as a percentage of this value in the last column.

There are similarities and differences in the amino acid sequences of NGF, NT-3 and BDNF. Most apparently, the mature protein factors are quite homologous (> 50%) especially when compared to the precursor portions of each preproprotein. (~ 20% homology).

Some major differences are observed when comparing the three precursors. First, NGF and NT-3 contain the dibasic

pair Lys-Arg at the primary processing site while BDNF contains an Arg-Arg pair. Secondly, only NGF and NT3 contain upstream dibasic sites (Arg-Arg); NGF has two sites whereas NT-3 has only one and BDNF does not have any.

5 Cell culture with proteases Kex2, mPC1, and mPC2

Plasmids pRK5.BDNF and pRK5.NT-3 were transfected as above with the exception that an additional 3 µg of expression plasmid pRK.Kex2, pRK.mPC1, or pRK.mPC2 DNA per plate (100mm) was added to the transfection mixture. Given  
10 the difference in the dibasic cleavage pattern with each precursor, the effects of the enzymes, Kex2, mPC1 and mPC2 on NT-3 and BDNF were examined.

Kex2 cleaved the upstream Arg-Arg site in NT-3, but was unable to process the BDNF upstream region because  
15 there is no such site.

mPC1 and mPC2 have no additional effect on the processing of NT-3 or BDNF in the 293 cells.

EXAMPLE 7

Construction of proinsulin B10 Histidine to  
20 Aspartic Acid mutant and insulin expression in transfected 293 cells.

The cDNA clone of the human preproinsulin gene, pSVEHIGDHFR, described in Australian patent 616,201 issued February 18, 1992, provided the coding sequence of the  
25 human preproinsulin gene for the final mammalian expression vector. A second source of the human preproinsulin gene, pH13 (Sures et al. *Science* 208:57-59 [1980]) has also been used in experiments to provide the coding sequence of human proinsulin. Aliquots (5-10 µL) of pSVEHIGDHFR were used  
30 for amplification of the coding region by RACE-PCR (rapid amplification of cDNA ends, Frohman 1988; Innis 1990) using a combination of gene-specific PCR primers: for the 5' end they were CAT AAG CTT ACC ATG GCC CTG TGG ATG CGC (sequence given 5' to 3') and for the 3' end they were CAT TCT AGA  
35 CTA GTT GCA GTA GTT CTC CAG (sequence given 5' to 3'). All PCR cloning reactions were carried out with Vent DNA polymerase (New England Biolabs) to minimize the introduction of mismatched bases during amplification of template. All proinsulin clones were sequenced with the

Sequenase 2.0 kit from USB and cloned into restriction digested pRK5. The final preproinsulin mammalian vector is pRK7.proins.

A human proinsulin mutant having a non-naturally occurring prohormone convertase cleavage site is constructed by mutating the human proinsulin cDNA, pRK.proins, encoding the naturally occurring basic cleavage site at the B-chain/C-peptide junction (KTRR) and A-chain/C-peptide junction (LQKR) by site-directed mutagenesis (Kunkel *Supra*). The double proinsulin variant, proins.RTKR.Ip/RQKR.IIp, was constructed. Ip is the Type I enzyme cleavage site and IIp is the Type II enzyme cleavage site. Primers used in construction of the proinsulin mutant, proins.RTKR.Ip/RQKR.IIp, are described in example 4. The double proinsulin mutant proins.RTKR.Ip/RQKR.IIp changes the native human proinsulin residue Lys 29 to Arg 29 at the Type I enzyme cleavage site, residue Arg 31 to Lys 31 at the Type I enzyme cleavage site and proinsulin residue Leu 62 is changed to Arg 62 at the Type II enzyme cleavage site. Other proinsulin mutants, proins.RTKR.Ip, proins.RQKR.IIp, proins.KR.Ip/RQKR.IIp, and proins.KTKR.Ip were constructed as in example 4. All mutants were screened through the primer regions with the Sequenase 2.0 kit from USB.

Proinsulin, pRK7.proins, and the proinsulin mutant, proins.RTKR.Ip/RQKR.IIp, were then mutagenized by the site-directed mutagenesis of Kunkel et al. (Methods Enzymol. vol.154, pg. 367-382 [1987]) to yield pRK7.proins.B10H>D, proinsulin having the histidine at position 10 in the B-chain replaced with an aspartic acid, and the proinsulin mutant, proins.RTKR.Ip/RQKR.IIp.B10H>D having the histidine at position 10 in the B-chain replaced with an aspartic acid. The primer used in the Kunkel et al. *Supra.* method was GC-TTC-CAC-CAG-GTC-GGA-TCC-GCA-CAG-GTG, with the sequence given in a 5' to 3' direction. All mutants were screened through the primer regions with the Sequenase 2.0 kit from USB.

DNA from the proinsulin mutants, proins.RTKR.Ip/RQKR.IIp, proins.RTKR.Ip/RQKR.IIp.B10H>D,

PRK7.proins.B10H>D, and proinsulin, PRK7.proins. was CsCl banded and used for human embryonic kidney cell line 293 (ATCC CRL 1573) transient transfection by the method of Gorman (Gorman DNA Prot Eng Tech 2:3-10, 1990). Cells were  
5 labelled as described by Gorman, *Supra* and cells and lysates were analyzed for insulin-like proteins. Protein-A sepharose immunoprecipitation was performed by the method of Harlow and Lane (from Antibodies: A Laboratory Manual, pub. Cold Spring Harbor Laboratory, chapter 11, pp. 421-470  
10 [1988]) on both supernatant and lysate samples using concentrated guinea pig anti-human insulin antibodies (Biomed I 01). Immunoprecipitation products were resuspended in either 2X Tris-Glycine Sample Buffer (from Novex)/8M urea plus b-mercaptoethanol or 2X Tricine buffer  
15 plus b-mercaptoethanol, heated for 5 minutes at 100 °C, spun briefly, and run reduced on 18% Tris-glycine SDS or 16% Tricine gels, respectively, according to manufacturer's directions (Novex). The gels were fixed (10% acetic acid, 25% isopropanol, 65% water), and soaked with Amplify  
20 (Amersham) as suggested in the instructions. Fixed, dried gels were exposed to film at -70 °C for 1 to 4 days.

DNA from the proinsulin mutants was used for transient transfection by the method of Gorman *Supra* and twelve to sixteen hours post transfection, the transfection media was  
25 replaced with serum free media and secretion products were collected for 36-56 hours. Processed insulin was measured in the collected supernatants by radioimmunoassay (RIA) using the Equate® RIA INSULIN, kit from Binax, Inc. according to the provided instructions.

30 To detect the bioactivity and specific activity of proinsulin or mutant proinsulin, secretion products were measured by quantitating the increase in tyrosine phosphorylation of the beta chain of the insulin receptor in 293 cells. 293 cells were plated in 24-well Costar  
35 plates in F12-DMEM medium containing serum (10%) (50,000 cells per well) and allowed to attach overnight. Cells were transferred into medium without serum for 8-16 hours. Serum free media was aspirated and cells were stimulated with 1 mL of various concentrations of wildtype bovine

insulin (Novo Industri A/S) or mutant insulin from conditioned supernatants. After a 10-15 minute incubation at 37°C, the reaction was stopped by the addition of 100 µl 2X Tris-Glycine sample buffer (from Novex) plus b-mercaptoethanol (50 µl per mL of sample buffer). The samples were vortexed vigorously, heated for 5 minutes at 100°C and 20µL was electrophoresed on an 8% Tris-Glycine SDS gel (Novex). After electrophoresis, tyrosine phosphorylation of the b chain of the insulin receptor was detected and quantitated by immunoblotting with anti-phosphotyrosine antibodies followed by scanning densitometry as described by Holmes et al. Science 256:1205-1210 [1992]).

NIH 3T3 HIR3.5 cells (Whitaker et al. PNAS USA, 84: 5237-5249 [1987]) overexpressing the human insulin receptor were incubated in serum free medium with various concentrations of unlabelled wildtype insulin or insulin mutant and a constant amount of <sup>125</sup>I-labelled Insulin (Amersham) for 16 hours at 4 °C. Unbound ligand was removed and cells were washed with ice cold medium. The amount of radioactivity bound was determined after solubilizing the cells with 0.1 N NaOH containing SDS (0.1%). Relative binding of wildtype insulin and the insulin mutants was determined using a non-linear regression program.

Determination of insulin receptor binding was determined by the following method: Human kidney cells (293) or 3T3 cells overexpressing the human insulin receptor, Whitaker et al. Supra were plated at about 100,000 cell per well dishes. One to two days after plating, the cells were washed in PBS and starved for 8-16 hours in binding buffer (F12/DMEM (50/50); 2mM Gln; 10 mM HEPES; 1 mg/ml BSA; penicillin and streptomycin (Gibco 600-5140 Ag 100 units/ml). Cells were placed on ice and washed twice with cold binding buffer. 480µl of non-radioactive insulin ligand (mutants or standards) in triplicate were placed in each well followed by 20µl (50,000-100,000 cpm/well) <sup>125</sup>I -labelled insulin (at tyrosine-A14) (Amersham). Cells were incubated at 4°C for 14-16 hours

with gentle rocking. The media was removed and cells were washed twice with cold binding buffer. The amount of radioactivity bound was determined after solubilizing the cells with 0.1N NaOH containing SDS (0.1%). A standard curve was generated using 0 to 1000nM human insulin standards (USP) or bovine standards (Novo Industri A/S). Relative binding of the insulin mutants was determined using a non-linear binding regression program.

## RESULTS

10 RIA Results In 293

smp1.	dil.	CPM	conc(uU)	construct	ng/mL
A	1:5	1111	GTS*	PRK7.proins	----
A	1:10	2111	1500-3000	PRK7.proins	>63
A	1:20	LOST	2750	PRK7.proins	>63
B	1:5	LOST	----	PRK7.proins	----
B	1:10	2326	1500-3000	PRK7.proins	>63
B	1:50	3589	1500	PRK7.proins	63
C	1:2	1472	GTS	prK7.proins.1*	----
C	1:5	2770	675	prK7.proins.1	27
C	1:10	4464	600	prK7.proins.1	27
D	1:2	1405	GTS	prK7.proins.1	----
D	1:5	LOST	----	prK7.proins.1	----
D	1:10	4215	650	prK7.proins.1	27
E	1:10	LOST	----	prK7.proins.2*	----
E	1:100	2311	>15,000	prK7.proins.2	>625
E	1:500	LOST	----	prK7.proins.2	----
E	1:1000	6596	20,000	prK7.proins.2	833
F	1:10	495	GTS	prK7.proins.2	----
F	1:100	1471	GTS	prK7.proins.2	----
F	1:500	5011	25,000	prK7.proins.2	1041
F	1:1000	5552	35,000	prK7.proins.2	1458
G	1:10	LOST	---	prK7.proins.3*	----
G	1:100	5548	3500	prK7.proins.3	146
G	1:500	7023	5000	prK7.proins.3	208
G	1:1000	7055	8000	prK7.proins.3	333
H	1:10	2021	---	prK7.proins.3	----
H	1:100	LOST	---	prK7.proins.3	----
H	1:500	6828	7500	prK7.proins.3	312
H	1:1000	7255	7000	prK7.proins.3	291

I	no dil	LOST	---	control	----
I	1:5	LOST	---	control	----
J	no dil	LOST	---	control	----
J	1:5	7600	LTS*	control	----

\*PRK7.proins.1 is proins.RTKR.Ip/RQKR.IIp

\*PRK7.proins.2 is proins.B10 H>D.

\*PRK7.proins.3 is proins.RTKR.Ip/RQKR.IIp.B10H>D.

\*GTS is greater than standard

5 \*LTS is less than standard

#### RIA Results In 293

smple	dil.	CPM	conc(uU)	construct	ng/ml
1	1:10	1200	3000	PRK7.proins	125
1	1:50	2750	2750	PRK7.proins	115
2	1:10	lost	----	PRK7.proins	----
2	1:50	lost	----	PRK7.proins	----
3	no dil	1522	145	PRK7.proins.1*	6
3	1:3	2668	180	PRK7.proins.1	7.5
3	1:6	lost	----	PRK7.proins.1	----
4	no dil	1581	135	PRK7.proins.1	5
4	1:3	2951	156	PRK7.proins.1	6.5
4	1:6	4046	210?	PRK7.proins.1	8.7
5	1:10	542	GTS*	PRK7.proins.2*	----
5	1:50	1327	13,500	PRK7.proins.2	560
5	1:100	1582	20,000	PRK7.proins.2	833
6	1:10	667	GTS	PRK7.proins.2	----
6	1:50	1448	12,500	PRK7.proins.2	520
6	1:100	1470	22,000	PRK7.proins.2	916
7	1:10	366	GTS	PRK7.proins.3*	----
7	1:50	876	GTS	PRK7.proins.3	----
7	1:100	1176	GTS	PRK7.proins.3	>1125
8	1:10	467	GTS	PRK7.proins.3	----
8	1:50	931	GTS	PRK7.proins.3	----
8	1:100	1038	GTS	PRK7.proins.3	>1125
9	no dil	713	GTS	PRK7.proins.4*	----
9	1:3	927	GTS	PRK7.proins.4	----
9	1:6	1475	840	PRK7.proins.4	35
10	no dil	416	GTS	PRK7.proins.4	----

10	1:3	1079	GTS	PRK7.proins.4	----
10	1:6	1435	840	PRK7.proins.4	35
11	no dil	1297	245	PRK7.proins.5*	10-11
11	1:3	2686	195	PRK7.proins.5	10-11
11	1:6	3615	270	PRK7.proins.5	10-11
12	no dil	lost	----	PRK7.proins.5	10-11
12	1:3	1486	435	PRK7.proins.5	10-11
12	1:6	3807	270	PRK7.proins.5	10-11
13	no dil	840	GTS	PRK7.proins.6*	----
13	1:3	776	GTS	PRK7.proins.6	----
13	1:6	2468	420	PRK7.proins.6	17.5
14	no dil	740	GTS	PRK7.proins.6	----
14	1:3	1217	----	PRK7.proins.6	----
14	1:6	2368	420	PRK7.proins.6	17.5
15	1:5	931	GTS	PRK7.proins.7*	----
15	1:10	1672	2100	PRK7.proins.7	8.8
16,	all	5800	LTS*	control	0

- \* PRK7.proins.1 is proins.RTKR.Ip/RQKR.IIp
- \* PRK7.proins.2 is proins.B10 H>D.
- \* PRK7.proins.3 is proins.RTKR.Ip/RQKR.IIp.B10 H>D.
- \* PRK7.proins.4 is proins.RTKR.Ip
- \* PRK7.proins.5 is proins.RQKR.IIp
- 5 \* PRK7.proins.6 is proins.KR.Ip/RQKR.IIp
- \* PRK7.proins.7 is proins.KTKR.Ip
- \* GTS is greater than standard
- \* LTS is less than standard

#### 10 Expression of proinsulin

Following transfection with an expression vector carrying the wildtype proinsulin cDNA, 293 HEK cells synthesize and secrete uncleaved proinsulin with a molecular weight of 6.5 kD. Unprocessed, [<sup>35</sup>S]-labelled proinsulin is immunoprecipitated from both the cell lysate and the media using an insulin specific antibody. The unprocessed material migrates with the 6.5kD molecular marker. Mature insulin, when reduced, migrates similarly



to the A and B chains at 2.35 and 3.4 kD when compared to the two bands of the molecular weight protein standards.

#### Expression of Proinsulin Mutants

Proins.RTKR.Ip/RQKR.IIp is processed into products  
5 that co-migrate with the A and B chains of insulin as well as processing intermediates. When proins.RTKR.Ip or proins.RQKR.IIp, representing a mutant cleavage site at the B-/C-chain junction or the A-/C-chain junction respectively, are transfected, only one of the mature  
10 chains was detected along with intermediates. When the mutant cleavage site is at the A-/C-chain junction, the A chain is detected along with a slower migrating band consistent with the B-C intermediate. When the mutant cleavage site is at the B-/C-chain junction, the B chain is  
15 detected along with a faster migrating band consistent with the A-C intermediate. Intermediates disappear when the amount of 293 homologous-cell enzyme that recognizes the mutant cleavage sites is increased by cotransfection with an expression vector expressing the 293 homologous-cell  
20 enzyme. Proins.KTKR.Ip was resistant to cleavage by the 293 cell enzyme.

#### Detection of Bioactivity

When mature, active insulin binds to the A-chain of  
25 the insulin receptor outside the cell, tyrosine residues on the B-chain of the insulin receptor are autophosphorylated (Kasuga et al., Science, 215:185-186 [1982]) Therefore, insulin bioactivity was assayed by measuring the ability of the B-chain of the insulin receptor to become  
30 autophosphorylated. Phosphorylation of the B-chain can be visually observed on an immunoblot. Upon stimulation with increasing concentrations of bovine insulin, the B-chain is increasingly observed at a mass of 96 kD by probing with antiphosphotyrosine antibodies. A similar increase in B-  
35 chain phosphorylation is detected by stimulation with various concentrations of the insulin mutants, proins.RTKR.Ip/RQKR.IIp and proins.RTKR.Ip/RQKR.IIp.B10 H>D.

## Relative Specific Activity and Insulin Binding Studies

Relative specific activity was determined by quantitating the amount of phosphorylation stimulated by each insulin mutant compared to insulin standards. Both the proins.RTKR.Ip/RQKR.IIp and proins.RTKR.Ip/RQKR.IIp.B10 H>D have similar activity to the bovine insulin standards within experimental error. Insulin receptor binding studies indicated similar binding affinities to the wildtype insulin standards with both the proins.RTKR.Ip/RQKR.IIp and proins.RTKR.Ip/RQKR.IIp.B10 H>D insulin mutants.

### B10 H>D Insulin Mutants

The relative amount of secretion products detected from proins.RTKR.Ip/RQKR.IIp.B10 H>D is greatly increased as compared to proins.RTKR.Ip/RQKR.IIp which lacks the B10 His to Asp change. When quantitated by RIA, the increase in the amount of processed insulin ranges from 10-40 fold depending on transfection efficiency. In addition to an increase in the accumulation of active insulin due to proins.RTKR.Ip/RQKR.IIp.B10 H>D, there is an increase in the accumulation of processing intermediates with the B10H>D mutant in the wildtype proinsulin background. Transfection with wildtype proinsulin does not yield insulin A and B chains; however, transfection with proins.B10H>D does yield detectable insulin A and B chain.

The proins.RTKR.Ip/RQKR.IIp.B10 H>D and proins.RTKR.Ip/RQKR.IIp have the same specific activity as measured by B-chain phosphorylation and the same capacity for binding to the insulin receptor. The B10H>D mutation appears to be more resistant to intracellular proteases as well whether this mutation occurs in the wildtype proinsulin or within the proins.RTKR.Ip/RQKR.IIp mutation.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Genentech, Inc.  
Gorman, Cornelia M.,  
Marriott, Dave,  
Groskreutz, Debrya J.
- 10 (ii) TITLE OF INVENTION: Prohormone Convertase Transformed Cells  
and Polypeptide Synthesis
- (iii) NUMBER OF SEQUENCES: 54
- 15 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
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(C) CITY: South San Francisco  
(D) STATE: California  
20 (E) COUNTRY: USA  
(F) ZIP: 94080
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
25 (B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: patin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER:  
(B) FILING DATE: 04-DEC-1992  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: 07/887265  
(B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: 07/803631  
(B) FILING DATE: 06-DEC-1992
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45 (A) NAME: Adler, Carolyn R.  
(B) REGISTRATION NUMBER: 32,324  
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## (2) INFORMATION FOR SEQ ID NO:1:

- 55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2355 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2012 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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40 GGCGTGTTTG CATTAGCTTT GGAGGCTAAC CTGGATCTGA CCTGGAGAGA 1300  
CATGCAACAT CTGACTGTGC TCACCTCCAA GCGGAACCAG CTTTCATGATG 1350  
AGGTTTCATCA GTGGCGACGG AATGGGGTTG GCCTGGAATT TAATCACCTC 1400  
50 TTTGGCTACG GAGTCCTTGA TGCAGGTGCC ATGGTGAAAA TGGCTAAAGA 1450  
CTGGAAAACT GTTCCGGAGA GATTCCATTG TGTGGGAGGC TCTGTGCAGA 1500  
55 ACCCTGAAAA AATACCACCC ACCGGCAAGC TGGTACTGAC CCTCAAAACA 1550  
AATGCATGTG AGGGGAAGGA AAACCTCGTC CGCTACCTGG AGCACGTCCA 1600  
AGCTGTCATC ACAGTCAACG CGACCAGGAG AGGAGACCTG AACATCAACA 1650

5 TGACCTCCCC AATGGGCACC AAGTCCATTT TGCTGAGCCG GCGTCCCAGA 1700  
 GACGACGACT CCAAGGTGGG CTTTGACAAG TGGCCTTTCA TGACCACCCA 1750  
 10 CACCTGGGGG GAGGATGCCC GAGGGACCTG GACCTGGAG CTGGGGTTTG 1800  
 TGGGCAGTGC ACCACAGAAG GGGTTGCTGA AGGAATGGAC CCTGATGCTT 1850  
 15 CACGGCACAC AGAGCGCCCC ATACATCGAT CAGGTGGTGA GGGATTACCA 1900  
 GTCTAAGCTG GCCATGTCCA AGAAGCAGGA GCTGGAGGAA GAGCTGGATG 1950  
 20 AGGCTGTGGA GACAAGCCTG CAAAGTATCC TGAGAAAGAA CTAGGGCCAC 2000  
 GCTTCCGAAT TC 2012  
 25

## (2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Gln	Arg	Gly	Trp	Thr	Leu	Gln	Cys	Thr	Ala	Phe	Ala	Phe	1	5	10	15
Phe	Cys	Val	Trp	Cys	Ala	Leu	Ser	Ser	Val	Lys	Ala	Lys	Arg	Gln	20	25	30	
Phe	Val	Asn	Glu	Trp	Ala	Ala	Glu	Ile	Pro	Gly	Gly	Gln	Glu	Ala	35	40	45	
Ala	Ser	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Tyr	Asp	Leu	Leu	Gly	Gln	50	55	60	
Ile	Gly	Ser	Leu	Glu	Asn	His	Tyr	Leu	Phe	Lys	His	Lys	Ser	His	65	70	75	
Pro	Arg	Arg	Ser	Arg	Arg	Ser	Ala	Leu	His	Ile	Thr	Lys	Arg	Leu	80	85	90	
Ser	Asp	Asp	Asp	Arg	Val	Thr	Trp	Ala	Glu	Gln	Gln	Tyr	Glu	Lys	95	100	105	
Glu	Arg	Ser	Lys	Arg	Ser	Val	Gln	Lys	Asp	Ser	Ala	Leu	Asp	Leu	110	115	120	
Phe	Asn	Asp	Pro	Met	Trp	Asn	Gln	Gln	Trp	Tyr	Leu	Gln	Asp	Thr	125	130	135	

	Arg	Met	Thr	Ala	Ala	Leu	Pro	Lys	Leu	Asp	Leu	His	Val	Ile	Pro	
					140					145					150	
5	Val	Trp	Glu	Lys	Gly	Ile	Thr	Gly	Lys	Gly	Val	Val	Ile	Thr	Val	
					155					160					165	
	Leu	Asp	Asp	Gly	Leu	Glu	Trp	Asn	His	Thr	Asp	Ile	Tyr	Ala	Asn	
					170					175					180	
10	Tyr	Asp	Pro	Glu	Ala	Ser	Tyr	Asp	Phe	Asn	Asp	Asn	Asp	His	Asp	
					185					190					195	
	Pro	Phe	Pro	Arg	Tyr	Asp	Leu	Thr	Asn	Glu	Asn	Lys	His	Gly	Thr	
					200					205					210	
15	Arg	Cys	Ala	Gly	Glu	Ile	Ala	Met	Gln	Ala	Asn	Asn	His	Lys	Cys	
					215					220					225	
20	Gly	Val	Gly	Val	Ala	Tyr	Asn	Ser	Lys	Val	Gly	Gly	Ile	Arg	Met	
					230					235					240	
	Leu	Asp	Gly	Ile	Val	Thr	Asp	Ala	Ile	Glu	Ala	Ser	Ser	Ile	Gly	
					245					250					255	
25	Phe	Asn	Pro	Gly	His	Val	Asp	Ile	Tyr	Ser	Ala	Ser	Trp	Gly	Pro	
					260					265					270	
	Asn	Asp	Asp	Gly	Lys	Thr	Val	Glu	Gly	Pro	Gly	Arg	Leu	Ala	Gln	
					275					280					285	
30	Lys	Ala	Phe	Glu	Tyr	Gly	Val	Lys	Gln	Gly	Arg	Gln	Gly	Lys	Gly	
					290					295					300	
35	Ser	Ile	Phe	Val	Trp	Ala	Ser	Gly	Asn	Gly	Gly	Arg	Gln	Gly	Asp	
					305					310					315	
	Asn	Cys	Asp	Cys	Asp	Gly	Tyr	Thr	Asp	Ser	Ile	Tyr	Thr	Ile	Ser	
					320					325					330	
40	Ile	Ser	Ser	Ala	Ser	Gln	Gln	Gly	Leu	Ser	Pro	Trp	Tyr	Ala	Glu	
					335					340					345	
	Lys	Cys	Ser	Ser	Thr	Leu	Ala	Thr	Ser	Tyr	Ser	Ser	Gly	Asp	Tyr	
					350					355					360	
45	Thr	Asp	Gln	Arg	Ile	Thr	Ser	Ala	Asp	Leu	His	Asn	Asp	Cys	Thr	
					365					370					375	
50	Glu	Thr	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala	Pro	Leu	Ala	Ala	Gly	
					380					385					390	
	Ile	Phe	Ala	Leu	Ala	Leu	Glu	Ala	Asn	Pro	Asn	Leu	Thr	Trp	Arg	
					395					400					405	
55	Asp	Met	Gln	His	Leu	Val	Val	Trp	Thr	Ser	Glu	Tyr	Asp	Pro	Leu	
					410					415					420	
	Ala	Ser	Asn	Pro	Gly	Trp	Lys	Lys	Asn	Gly	Ala	Gly	Leu	Met	Val	
					425					430					435	
60	Asn	Ser	Arg	Phe	Gly	Phe	Gly	Leu	Leu	Asn	Ala	Lys	Ala	Leu	Val	
					440					445					450	

	Asp	Leu	Ala	Asp	Pro	Arg	Thr	Trp	Arg	Asn	Val	Pro	Glu	Lys	Lys	
					455					460					465	
5	Glu	Cys	Val	Val	Lys	Asp	Asn	Asn	Phe	Glu	Pro	Arg	Ala	Leu	Lys	
					470					475					480	
	Ala	Asn	Gly	Glu	Val	Ile	Val	Glu	Ile	Pro	Thr	Arg	Ala	Cys	Glu	
					485					490					495	
10	Gly	Gln	Glu	Asn	Ala	Ile	Lys	Ser	Leu	Glu	His	Val	Gln	Phe	Glu	
					500					505					510	
	Ala	Thr	Ile	Glu	Tyr	Ser	Arg	Arg	Gly	Asp	Leu	His	Val	Thr	Leu	
					515					520					525	
15	Thr	Ser	Ala	Val	Gly	Thr	Ser	Thr	Val	Leu	Leu	Ala	Glu	Arg	Glu	
					530					535					540	
	Arg	Asp	Thr	Ser	Pro	Asn	Gly	Phe	Lys	Asn	Trp	Asp	Phe	Met	Ser	
20					545					550					555	
	Val	His	Thr	Trp	Gly	Glu	Asn	Pro	Val	Gly	Thr	Trp	Thr	Leu	Lys	
					560					565					570	
25	Ile	Thr	Asp	Met	Ser	Gly	Arg	Met	Gln	Asn	Glu	Gly	Arg	Ile	Val	
					575					580					585	
	Asn	Trp	Lys	Leu	Ile	Leu	His	Gly	Thr	Ser	Ser	Gln	Pro	Glu	His	
					590					595					600	
30	Met	Lys	Gln	Pro	Arg	Val	Tyr	Thr	Ser	Tyr	Asn	Thr	Val	Gln	Asn	
					605					610					615	
	Asp	Arg	Arg	Gly	Val	Glu	Lys	Met	Val	Asn	Val	Val	Glu	Lys	Arg	
35					620					625					630	
	Pro	Thr	Gln	Lys	Ser	Leu	Asn	Gly	Asn	Leu	Leu	Val	Pro	Lys	Asn	
					635					640					645	
40	Ser	Ser	Ser	Ser	Asn	Val	Glu	Gly	Arg	Arg	Asp	Glu	Gln	Val	Gln	
					650					655					660	
	Gly	Thr	Pro	Ser	Lys	Ala	Met	Leu	Arg	Leu	Leu	Gln	Ser	Ala	Phe	
					665					670					675	
45	Ser	Lys	Asn	Ala	Leu	Ser	Lys	Gln	Ser	Pro	Lys	Lys	Ser	Pro	Ser	
					680					685					690	
	Ala	Lys	Leu	Ser	Ile	Pro	Tyr	Glu	Ser	Phe	Tyr	Glu	Ala	Leu	Glu	
50					695					700					705	
	Lys	Leu	Asn	Lys	Pro	Ser	Lys	Leu	Glu	Gly	Ser	Glu	Asp	Ser	Leu	
					710					715					720	
55	Tyr	Ser	Asp	Tyr	Val	Asp	Val	Phe	Tyr	Asn	Thr	Lys	Pro	Tyr	Lys	
					725					730					735	
	His	Arg	Asp	Asp	Arg	Leu	Leu	Gln	Ala	Leu	Met	Asp	Ile	Leu	Asn	
					740					745					750	
60	Glu	Glu	Asn													
					753											

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 637 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

10 Met Glu Gly Gly Cys Gly Ser Gln Trp Lys Ala Ala Gly Phe Leu
    1           5           10           15
    Phe Cys Val Met Val Phe Ala Ser Ala Glu Arg Pro Val Phe Thr
    20           25           30
15 Asn His Phe Leu Val Glu Leu His Lys Asp Gly Glu Glu Glu Ala
    35           40           45
    Arg Gln Val Ala Ala Glu His Gly Phe Gly Val Arg Lys Leu Pro
    50           55           60
    Phe Ala Glu Gly Leu Tyr His Phe Tyr His Asn Gly Leu Ala Lys
    65           70           75
25 Ala Lys Arg Arg Arg Ser Leu His His Lys Arg Gln Leu Glu Arg
    80           85           90
    Asp Pro Arg Ile Lys Met Ala Leu Gln Gln Glu Gly Phe Asp Arg
    95           100          105
30 Lys Lys Arg Gly Tyr Arg Asp Ile Asn Glu Ile Asp Ile Asn Met
    110          115          120
    Asn Asp Pro Leu Phe Thr Lys Gln Trp Tyr Leu Phe Asn Thr Gly
    125          130          135
    Gln Ala Asp Gly Thr Pro Gly Leu Asp Leu Asn Val Ala Glu Ala
    140          145          150
40 Trp Glu Leu Gly Tyr Thr Gly Lys Gly Val Thr Ile Gly Ile Met
    155          160          165
    Asp Asp Gly Ile Asp Tyr Leu His Pro Asp Leu Ala Tyr Asn Tyr
    170          175          180
45 Asn Ala Asp Ala Ser Tyr Asp Phe Ser Ser Asn Asp Pro Tyr Pro
    185          190          195
    Tyr Pro Arg Tyr Thr Asp Asp Trp Phe Asn Ser His Gly Thr Arg
    200          205          210
50 Cys Ala Gly Glu Val Ser Ala Ala Ala Ser Asn Asn Ile Cys Gly
    215          220          225
    Val Gly Val Ala Tyr Asn Ser Lys Val Ala Gly Ile Arg Met Leu
    230          235          240
    Asp Gln Pro Phe Met Thr Asp Ile Ile Glu Ala Ser Ser Ile Ser
    245          250          255
60 His Met Pro Gln Leu Ile Asp Ile Tyr Ser Ala Ser Trp Gly Pro
    260          265          270

```



	Thr Asp Asn Gly Lys Thr Val Asp Gly Pro Arg Glu Leu Thr Leu	275	280	285
5	Gln Ala Met Ala Asp Gly Val Asn Lys Gly Arg Gly Gly Lys Gly	290	295	300
	Ser Ile Tyr Val Trp Ala Ser Gly Asp Gly Gly Ser Tyr Asp Asp	305	310	315
10	Cys Asn Cys Asp Gly Tyr Ala Ser Ser Met Trp Thr Ile Ser Ile	320	325	330
	Asn Ser Ala Ile Asn Asp Gly Arg Thr Ala Leu Tyr Asp Glu Ser	335	340	345
15	Cys Ser Ser Thr Leu Ala Ser Thr Phe Ser Asn Gly Arg Lys Arg	350	355	360
20	Asn Pro Glu Ala Gly Val Ala Thr Thr Asp Leu Tyr Gly Asn Cys	365	370	375
	Thr Leu Arg His Ser Gly Thr Ser Ala Ala Ala Pro Glu Ala Ala	380	385	390
25	Gly Val Phe Ala Leu Ala Leu Glu Ala Asn Leu Asp Leu Thr Trp	395	400	405
	Arg Asp Met Gln His Leu Thr Val Leu Thr Ser Lys Arg Asn Gln	410	415	420
30	Leu His Asp Glu Val His Gln Trp Arg Arg Asn Gly Val Gly Leu	425	430	435
	Glu Phe Asn His Leu Phe Gly Tyr Gly Val Leu Asp Ala Gly Ala	440	445	450
35	Met Val Lys Met Ala Lys Asp Trp Lys Thr Val Pro Glu Arg Phe	455	460	465
40	His Cys Val Gly Gly Ser Val Gln Asn Pro Glu Lys Ile Pro Pro	470	475	480
	Thr Gly Lys Leu Val Leu Thr Leu Lys Thr Asn Ala Cys Glu Gly	485	490	495
45	Lys Glu Asn Phe Val Arg Tyr Leu Glu His Val Gln Ala Val Ile	500	505	510
	Thr Val Asn Ala Thr Arg Arg Gly Asp Leu Asn Ile Asn Met Thr	515	520	525
50	Ser Pro Met Gly Thr Lys Ser Ile Leu Leu Ser Arg Arg Pro Arg	530	535	540
	Asp Asp Asp Ser Lys Val Gly Phe Asp Lys Trp Pro Phe Met Thr	545	550	555
	Thr His Thr Trp Gly Glu Asp Ala Arg Gly Thr Trp Thr Leu Glu	560	565	570
60	Leu Gly Phe Val Gly Ser Ala Pro Gln Lys Gly Leu Leu Lys Glu	575	580	585

Trp Thr Leu Met Leu His Gly Thr Gln Ser Ala Pro Tyr Ile Asp  
 590 600

5 Gln Val Val Arg Asp Tyr Gln Ser Lys Leu Ala Met Ser Lys Lys  
 605 610 615

Gln Glu Leu Glu Glu Glu Leu Asp Glu Ala Val Glu Arg Ser Leu  
 620 625 630

10 Gln Ser Ile Leu Arg Lys Asn  
 635 637

## (2) INFORMATION FOR SEQ ID NO:5:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 GCAAAATCTA GAYKGCNATY GTNGAYGAKG GN 32

## (2) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40 AAGCATGAGC TCNGGRGCRG CRGCNGANCC 30

## (2) INFORMATION FOR SEQ ID NO:7:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55 GATATCACTC AGATCGATGA ATTCGAGCTC 30

## (2) INFORMATION FOR SEQ ID NO:8:

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5

AAGCTTTCTA GAGGATCCCT CTGCTGGATT TGG 33

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20

AAGCTTGAAT TCTCCAACCC CACACTTGTG 30

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

AGATCGATGA ATTGAGCTC 20

40 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: nucleic acid

45 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50

CATTCTCGAA AAAAGAGACA A 21

55 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CATTCTGTAA AAAAGAGACA A 21

5

(2) INFORMATION FOR SEQ ID NO:13:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATTCTAGAG CAAAGAGACA A 21

20

(2) INFORMATION FOR SEQ ID NO:14:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CATTCTAGAA AAGCAAGACA A 21

35

(2) INFORMATION FOR SEQ ID NO:15:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATTCTAGAA AAAGAGCACA A 21

50

(2) INFORMATION FOR SEQ ID NO:16:

- 55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCTGGAGCA AAGCTTCTCT G 21

## (2) INFORMATION FOR SEQ ID NO:17:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

15 ACCTGGAGCG CTAGGTCTCT G 21

## (2) INFORMATION FOR SEQ ID NO:18:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

30 CATAAGCTTA CCATGGCCCT GTGGATGCCG 30

## (2) INFORMATION FOR SEQ ID NO:19:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

45 CATTCTAGAC TAGTTGCAGT AGTTCTCCAG 30

## (2) INFORMATION FOR SEQ ID NO:20:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Thr Arg Arg

1

4

60

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Gln Lys Arg  
1 4

10 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Thr Lys Arg  
20 1 4

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30 Arg Gln Lys Arg  
1 4

(2) INFORMATION FOR SEQ ID NO:24:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Thr Lys Arg  
1 4

45 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 31 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

55 CTCTGCCTCC CGCTTGGTCC TGGGTGTGTA G 31

60 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CACGCTTCTG CCGGGATCCC TC 22

10

(2) INFORMATION FOR SEQ ID NO:27:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCTGCCTCC CGCTTGGTCT TCGGTGTGTA G 31

25

(2) INFORMATION FOR SEQ ID NO:28:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATATGAAGA GCAGATCTTT TGGACCTCCG AGGATG 36

40

(2) INFORMATION FOR SEQ ID NO:29:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTTATGGTGT AAGCTTCGTT TTGCTCTGGC CTTTGCAAG 39

55

(2) INFORMATION FOR SEQ ID NO:30:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

5

TACAACTCAC CGCGGGTCCT G 21

10 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

20

AAGATGGGAT GGGATGATGA CCGTTTCCGC CTTGATGT 38

25 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35

ACATCACGGC GGAAACGGTC ATCATCCCAT CCCATCTT 38

40 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: nucleic acid

45 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50

GATATAAGCT TGAGAGTGTA GAAGGGGC 28

55 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 bases

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:



GGCTTGACAT CATGGGCTGA CACTTTCGAA CACATGATAG 40

5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 41 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGATGGGAT GGGATGATGA GCGCCGGACC CTCATGGACA T 41

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 41 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGTCCATGA GGGTCCGGCG CTCATCATCC CATCCCATCT T 41

35

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 28 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATATAAGCT TGAGAGTGTA GAAGGGGC 28

50

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 51 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGAGCGACAG CACCCCTTG GAGCCCCGC CCTTGATCT CATGGAGGAT 50

T 51

5

(2) INFORMATION FOR SEQ ID NO:39:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCAGCTCCCC TCGTCGGGCG GGTCCGAGT GCCGTTTCCG CCGTGATGTT 50

20

C 51

25 (2) INFORMATION FOR SEQ ID NO:40:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

35

ACGTGGGCAG CCCCGTGGTG GCGAACAGAA CATCACGGCG GAAACGGC 48

40 (2) INFORMATION FOR SEQ ID NO:41:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

50

TGTTGCCAC CACGGGGCTG CCCACGTAAT CCTCCATGAG ATACAAGG 48

55 (2) INFORMATION FOR SEQ ID NO:42:

60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTCGGACCCC GCCCGACGAG GGGAGC 26

5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GCGGGGGCTC CAAGGGGGTG CTGTGCG 27

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTAGAACAAC ATGGACATGG TGGCAATATT GTCGACTCTG GAGTCGACCT 50

35

GCAG 54

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

50

CACATAAAAC AAGATGGACA TGGTCTTGTT CACCTGTAGG ATCCCCGG 48

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 bases  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AGTAAGGAAA AGGATGGTCA TGCTGGAGGT CGACAAGCTT GAGAATTCAA 50

5

TCG 53

## 10 (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Xaa Xaa Xaa Arg

20

1 4

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

30

His Ser Arg Lys Lys Arg Gln  
1 5 7

## (2) INFORMATION FOR SEQ ID NO:49:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

His Ser Val Lys Lys Arg Gln  
1 5 7

45

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

55

His Ser Arg Ala Lys Arg Gln  
1 5 7

## (2) INFORMATION FOR SEQ ID NO:51:

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

5 His Ser Arg Lys Ala Arg Gln  
1 5 7

(2) INFORMATION FOR SEQ ID NO:52:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

15 His Ser Arg Lys Arg Ala Gln  
1 5 7

(2) INFORMATION FOR SEQ ID NO:53:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

30 Thr Trp Ser Lys Ala Ser Gln  
1 5 7

(2) INFORMATION FOR SEQ ID NO:54:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

40 Thr Trp Ser Ala Arg Ser Gln  
1 5 7

45

We claim:

1. A method for the production of a heterologous polypeptide factor in a polypeptide factor-dependent host cell comprising:
  - 5 a) introducing into the polypeptide factor-dependent host cell nucleic acid encoding a heterologous polypeptide factor precursor comprising a cleavage site heterologous to the polypeptide factor and recognizable by a host cell enzyme and wherein said host cell is dependent on the  
10 cleavage product of said polypeptide factor precursor; and
  - b) culturing said host cell under conditions wherein the polypeptide factor precursor is expressed and cleaved at said cleavage site by the host cell enzyme, thereby producing said polypeptide factor  
15
2. The method of claim 1, wherein said cleavage site recognizable by said host cell is a prohormone hormone convertase cleavage site.
- 20 3. The method of claim 2 wherein said prohormone convertase cleavage site is ZXZR (Seq ID #47), wherein Z is LYS or ARG; X is any amino acid; and R is ARG.
4. The method of claim 1 wherein said host cell is  
25 mammalian.
5. The method of claim 4 wherein said host cell is a chinese hamster ovary cell.
- 30 6. The method of claim 1 further comprising introducing into said host cell nucleic acid encoding a selectable gene.
7. The method of claim 1 wherein said polypeptide factor  
35 precursor is proinsulin and said polypeptide factor is insulin.
8. The method of claim 7 wherein said nucleic acid encoding proinsulin is operably linked to a promoter.

9. The method of claim 8 wherein said promoter is inducible.

10. The method of claim 1 wherein said nucleic acid  
5 encoding a polypeptide factor precursor is proins.RTKR.Ip/RQKR.IIp.

11. The method of claim 1 wherein said nucleic acid  
encoding a polypeptide factor precursor is  
10 proins.RTKR.Ip/RQKR.IIp.B10 H>D.

12. The method of claim 1 comprising the additional steps:

a) further introducing into the host cell nucleic acid encoding a desired polypeptide; and

15 b) culturing said host cell under conditions wherein said desired polypeptide is expressed.

13. The method of claim 12 wherein said desired polypeptide is selected from the group comprising: relaxin,  
20 insulin-like growth factor I and II, growth hormone; factor VIII; factor IX; tumor necrosis factor-alpha and -beta; tissue factor protein; inhibin; activin; vascular endothelial growth factor; thrombopoietin; nerve growth factor; platelet-derived growth factor; fibroblast growth  
25 factor; epidermal growth factor; transforming growth factor; insulin-like growth factor-I and -II; interferon; GM-CSF; G-CSF; interleukin; decay accelerating factor; and atrial natriuretic peptides A, B or C.

30 14. The method of claim 12 further comprising recovering said desired polypeptide

15. The method of claim 12 wherein said desired polypeptide further comprises a precursor region having a  
35 second cleavage site recognizable by a host cell enzyme and wherein the precursor is cleaved at said second cleavage site by the host cell enzyme, thereby producing said desired polypeptide.

16. The method of claim 1 comprising the additional steps:  
a) further introducing into the host cell nucleic acid encoding said host cell enzyme; and

b) culturing said host cell under conditions wherein  
5 said host cell enzyme is expressed.

17. A method for producing a desired polypeptide in a host cell, comprising:

a) introducing into the host cell nucleic acid  
10 encoding the desired polypeptide precursor having a cleavage site not recognizable by any endogenous host cell enzyme and recognizable by enzyme heterologous to said host cell;

b) introducing into said host cell nucleic acid  
15 encoding the enzyme heterologous to said host cell and wherein said enzyme heterologous to said host cell further comprises a precursor having a cleavage site recognizable by a host cell enzyme, and

c) culturing said host cell under conditions wherein  
20 said precursor of enzyme heterologous to said host cell is expressed and cleaved at said cleavage site by host cell enzyme thereby producing said heterologous enzyme and wherein said desired polypeptide precursor is expressed and cleaved at said cleavage site by said enzyme heterologous  
25 to said host cell thereby producing said desired polypeptide.

18. The method of claim 17 further comprising recovering  
said desired polypeptide.

30

19. The method of claim 17 wherein the desired polypeptide is relaxin, growth hormone; factor VIII; factor IX; tumor necrosis factor-alpha and -beta; tissue factor protein; inhibin; activin; vascular endothelial growth factor;  
35 thrombopoietin; nerve growth factor; platelet-derived growth factor; fibroblast growth factor; epidermal growth factor; transforming growth factor; insulin-like growth factor-I and -II; interferon; GM-CSF; G-CSF; interleukin;



decay accelerating factor; and atrial natriuretic peptides A, B or C.

20. The method of claim 17 wherein the enzyme heterologous  
5 to said host cell is a prohormone convertase.

21. The method of claim 20 wherein said prohormone  
convertase is mammalian prohormone convertase 1 or  
mammalian prohormone convertase 2.

10

22. The method of claim 17 wherein said host cell is a  
polypeptide-factor dependent host cell.

23. The method of claim 22 further comprising introducing  
15 into the polypeptide factor-dependent host cell nucleic  
acid encoding a heterologous polypeptide factor precursor  
further comprising a cleavage site recognizable by a host  
cell enzyme or a heterologous enzyme added to said host  
cell, and culturing said host cell under conditions wherein  
20 the polypeptide factor precursor is cleaved at the cleavage  
site thereby producing said polypeptide factor.

24. The method of claim 23 wherein said polypeptide factor  
precursor is encoded by proins.RTKR.Ip/RQKR.IIp.B10 H>D.

25

25. The method of claim 17 further comprising introducing  
into the host cell nucleic acid encoding a selectable gene.

26. The method of claim 17 wherein said host cell is  
30 mammalian.

27. The isolated proinsulin encoded by the nucleic acid,  
proins.RTKR.Ip/RQKR.IIp.B10 H>D.

35 28. The isolated nucleic acid proins.RTKR.Ip/RQKR.IIp.B10  
H>D.

**FIG. 1A**

TCTAGATCTA GCTGGTGTGT CTCTGATCTT GCTTCTTTTC TCCCAGCCCT 50

TCCTACTTGT GTGAGAACAA GGTTTTGAGC CATGGAGCAA AGAGGTGGA 100

CTCTGCAGTG TACTGCTTTC GCCTTCTTTT GCGTTTGGTG TGCACTAAGC 150

AGTGTAAGAG CAAAGAGGCA GTTTGTTAAT GAATGGGCGG CGGAGATCCC 200

CGGAGGGCAA GAAGCTGCCT CTGCCATCGC CGAAGAACTG GGGTATGACC 250

TTTTGGGTCA GATTGGATCA CTTGAAAATC ACTATTTATT CAAACACAAA 300

AGCCATCCTC GGAGGTCCCG AAGAAGCGCT CTCATATCA CTAAGAGGTT 350

ATCTGATGAT GATCGTGTGA CGTGGGCTGA ACAACAGTAT GAAAAAGAGA 400

GAAGTAAACG TTCAGTTCAA AAAGACTCAG CATTGGATCT CTTCAATGAT 450

CCAATGTGGA ATCAGCAGTG GTACTTGCAA GATACCAGAA TGA CTGCAGC 500

TCTGCCCAAG CTGGACCTTC ATGTAATACC TGT TTGGGAA AAGGGTATTA 550

CTGGCAAAGG AGTTGTTATT ACTGTACTGG ATGATGGCTT GGAGTGAAT 600

CACACAGACA TTTATGCCAA TTATGATCCA GAGGCTAGCT ATGATTTTAA 650

CGATAATGAT CATGATCCAT TTCCCCGATA TGATCTCACA AATGAAAACA 700

AACATGGAAC AAGATGTGCA GGTGAAATTG CCATGCAAGC AAATAATCAC 750

AAGTGTGGGG TTGGAGTTGC ATATAATTCC AAAGTTGGAG GCATAAGAAT 800

**FIG. 1B**

GCTGGATGGC ATTGTAAGT ATGCCATTGA GGCTAGTTCA ATTGGATTCA 850

ACCCTGGCCA TGTGGATATT TACAGTGCAA GCTGGGGCCC TAATGATGAT 900

GGAAAACTG TGGAGGGGCC TGGCAGACTA GCCCAGAAGG CATTGAATA 950

TGGTGTCAA CAGGGGAGAC AAGGGAAAG CTCCATCTTT GTCTGGGCTT 1000

CAGGGAATGG GGGTCCTCAG GGAGATAACT GTGACTGTGA TGGCTACACA 1050

GACAGCATTT ACACCATCTC TATCAGCAGT GCCTCCCAGC AAGGCCTGTC 1100

ACCTTGGTAT GCAGAGAAGT GTTCTTCCAC ATTGGCTACC TCCTACAGCA 1150

GTGGTGATTA CACAGACCAG CGAATAACAA GCGCTGACCT GCACAATGAC 1200

TGCACAGAGA CCCACACAGG CACCTCGGCT TCAGCACCCC TGGCTGCTGG 1250

TATCTTTGCT CTGGCCTTGG AGGCAAACCC AAATCTTACC TGGAGAGATA 1300

TGCAGCATCT GGTGTCTGG ACCTCTGAGT ACGACCCATT GGCCAGTAAC 1350

CCAGGTTGGA AAAAGAATGG GGCAGGCTTG ATGGTGAACA GCCGATTG 1400

ATTGGCTTG CTAAATGCCA AAGCTCTGGT GGATTGGCT GATCCTCGGA 1450

CCTGGAGAAA TGTGCCTGAG AAGAAAGAAT GTGTTGTAAA AGACAATAAC 1500

TTTGAGCCTA GAGCCCTGAA AGCTAATGGA GAAGTAATTG TTGAAATCCC 1550

AACAAGAGCT TGTGAAGGAC AAGAAAATGC TATCAAGTCT CTGGAACATG 1600

TGCAATTGA AGCAACAATT GAATATTCTC GTAGAGGAGA CCTTCATGTC 1650

**FIG. 1C**

ACACTCACTT CTGCTGTTGG AACCAGCACT GTACTGTTGG CTGAAAGGGA 1700

AAGAGATACA TCCCCCAATG GCTTTAAGAA TTGGGACTTC ATGTCTGTTC 1750

ATACATGGGG AGAGAATCCT GTAGGCACCT GGACATTGAA AATTACAGAC 1800

ATGTCTGGAA GAATGCAAAA TGAAGGAAGG ATTGTGAACT GGAAGTTGAT 1850

TTTGCATGGG ACATCTTCTC AACCAGAGCA CATGAAGCAG CCCC GTGTGT 1900

ACACATCCTA CAATACAGTC CAGAATGACA GGAGAGGAGT GGAAAAGATG 1950

CCTGGTACCC AAAA ACTCCA GCAGCAGCAA TGTGGAGGGT AGAAGGGATG 2050

AGCAGGTACA AGGAACTCCT TCAAAGGCCA TGCTGCGACT CCTACAAAGT 2100

GCTTTTAGCA AGAATGCACT TTCAAAACAA TCACCAAAGA AGTCTCCAAG 2150

TGCAAAGCTC AGCATCCCTT ATGAAAGTTT CTATGAAGCC TTGGAAAAGC 2200

TTAACAAGCC CTCCAAGCTT GAAGGCTCTG AAGACAGTCT GTACAGTGAC 2250

TATGTTGATG TATTCTATAA CACAAAACCT TATAAGCATA GAGATGACAG 2300

GCTGCTGCAA GCTCTCATGG ACATCCTAAA TGAGGAGAAT TAAAATAAGG 2350

AGCTC 2355

**FIG. 2A**

TCTAGATGCA TCTTCCCTCT TCGTCCCCTG CTCCACCACC CTGCGCGCCT 50

CACAGCCCCG CTTTTCACCTC CCAAAGAAGG ATGGAGGGCG GTTGTGGATC 100

CCAGTGGAAG GCGGCCGGGT TCCTCTTCTG TGTGATGGTT TTTGCGTCTG 150

CCGAGAGACC CGTCTTCACG AATCATTTTC TTGTGGAGTT GCATAAAGAC 200

GGAGAGGAAG AGGCTCGCCA AGTTGCAGCA GAACACGGCT TTGGAGTCCG 250

AAAGCTCCCC TTTGCAGAAG GCCTGTATCA CTTTATCAC AATGGGCTTG 300

CAAAGGCCAA AAGAAGACGC AGCCTACACC ATAAGCGGCA GCTAGAGAGA 350

GACCCAGGA TAAAGATGGC GCTGCAACAA GAAGGATTTG ACCGTAAAAA 400

GAGAGGGTAC AGGGACATCA ATGAGATTGA CATCAACATG AATGATCCTC 450

TCTTTACAAA GCAATGGTAC CTGTTCAACA CTGGGCAAGC CGATGGA ACT 500

CCTGGGCTAG ACTTGAACGT GGCCGAAGCC TGGGAGCTGG GATACACAGG 550

AAAAGGAGTG ACCATTGGAA TTATGGATGA TGAATTGAC TATCTCCACC 600

CAGACCTGGC CTACA ACTAC AACGCTGATG CAAGTTATGA CTT CAGCAGC 650

AATGACCCCT ACCCATACCC TCGATACACA GATGACTGGT TCAACAGCCA 700

TGGA ACTAGG TGTGCAGGAG AAGTTTCTGC TGCAGCCAGC AACAATATCT 750

GTGGAGTCGG CGTAGCATAC AACTCCAAGG TGGCAGGGAT CCGGATGCTG 800

GACCAGCCCT TTATGACAGA CATCATCGAA GCCTCCTCCA TCAGCCACAT 850

**FIG. 2B**

GCCTCAACTG ATCGACATCT ACAGTGCAAG CTGGGGCCCC ACAGACAATG 900

GGAAGACGGT TGATGGGCCC CGAGAGCTCA CACTCCAGGC CATGGCTGAT 950

GGCGTGAACA AGGGCCGTGG GGGCAAAGGC AGCATCTATG TGTGGGCCTC 1000

TGGGGACGGT GGCAGCTACG ATGACTGCAA CTGTGACGGC TATGCTTCAA 1050

GCATGTGGAC CATCTCCATC AACTCAGCCA TCAATGATGG CAGGACTGCC 1100

TTGTATGATG AGAGTTGCTC TTCCACCTTA GCATCCACCT TCAGCAATGG 1150

GAGGAAGAGG AATCCTGAGG CTGGTGTGGC TACCACAGAC TTGTATGGCA 1200

ACTGTACTCT GAGACACTCT GGGACATCTG CAGCTGCTCC GGAGGCAGCT 1250

GGCGTGTTTG CATTAGCTTT GGAGGCTAAC CTGGATCTGA CCTGGAGAGA 1300

CATGCAACAT CTGACTGTGC TCACCTCCAA GCGGAACCAG CTTGATGATG 1350

AGGTTGATCA GTGGCGACGG AATGGGGTTG GCCTGGAATT TAATCACCTC 1400

TTTGGCTACG GAGTCCTTGA TGCAGGTGCC ATGGTGAAAA TGGCTAAAGA 1450

CTGGAAACT GTTCCGGAGA GATTCCATTG TGTGGGAGGC TCTGTGCAGA 1500

ACCCTGAAAA AATACCACCC ACCGGCAAGC TGGTACTGAC CCTCAAACA 1550

AATGCATGTG AGGGGAAGGA AAACCTCGTC CGCTACCTGG AGCACGTCCA 1600

AGCTGTCATC ACAGTCAACG CGACCAGGAG AGGAGACCTG AACATCAACA 1650

## FIG. 2C

TGACCTCCCC AATGGGCACC AAGTCCATTT TGCTGAGCCG GCGTCCCAGA 1700  
GACGACGACT CCAAGGTGGG CTTTGACAAG TGGCCTTTCA TGACCACCCA 1750  
CACCTGGGGG GAGGATGCCC GAGGGACCTG GACCCTGGAG CTGGGGTTTG 1800  
TGGGCAGTGC ACCACAGAAG GGGTTGCTGA AGGAATGGAC CCTGATGCTT 1850  
CACGGCACAC AGAGCGCCCC ATACATCGAT CAGGTGGTGA GGGATTACCA 1900  
GTCTAAGCTG GCCATGTCCA AGAAGCAGGA GCTGGAGGAA GAGCTGGATG 1950  
AGGCTGTGGA GAGAAGCCTG CAAAGTATCC TGAGAAAGAA CTAGGGCCAC 2000  
GCTTCCGAAT TC 2012

**FIG. 3A**

Met	Glu	Gln	Arg	Gly	Trp	Thr	Leu	Gln	Cys	Thr	Ala	Phe	Ala	Phe	1	5	10	15
Phe	Cys	Val	Trp	Cys	Ala	Leu	Ser	Ser	Val	Lys	Ala	Lys	Arg	Gln	20	25	30	
Phe	Val	Asn	Glu	Trp	Ala	Ala	Glu	Ile	Pro	Gly	Gly	Gln	Glu	Ala	35	40	45	
Ala	Ser	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Tyr	Asp	Leu	Leu	Gly	Gln	50	55	60	
Ile	Gly	Ser	Leu	Glu	Asn	His	Tyr	Leu	Phe	Lys	His	Lys	Ser	His	65	70	75	
Pro	Arg	Arg	Ser	Arg	Arg	Ser	Ala	Leu	His	Ile	Thr	Lys	Arg	Leu	80	85	90	
Ser	Asp	Asp	Asp	Arg	Val	Thr	Trp	Ala	Glu	Gln	Gln	Tyr	Glu	Lys	95	100	105	
Glu	Arg	Ser	Lys	Arg	Ser	Val	Gln	Lys	Asp	Ser	Ala	Leu	Asp	Leu	110	115	120	
Phe	Asn	Asp	Pro	Met	Trp	Asn	Gln	Gln	Trp	Tyr	Leu	Gln	Asp	Thr	125	130	135	
Arg	Met	Thr	Ala	Ala	Leu	Pro	Lys	Leu	Asp	Leu	His	Val	Ile	Pro	140	145	150	
Val	Trp	Glu	Lys	Gly	Ile	Thr	Gly	Lys	Gly	Val	Val	Ile	Thr	Val	155	160	165	
Leu	Asp	Asp	Gly	Leu	Glu	Trp	Asn	His	Thr	Asp	Ile	Tyr	Ala	Asn	170	175	180	
Tyr	Asp	Pro	Glu	Ala	Ser	Tyr	Asp	Phe	Asn	Asp	Asn	Asp	His	Asp	185	190	195	
Pro	Phe	Pro	Arg	Tyr	Asp	Leu	Thr	Asn	Glu	Asn	Lys	His	Gly	Thr	200	205	210	
Arg	Cys	Ala	Gly	Glu	Ile	Ala	Met	Gln	Ala	Asn	Asn	His	Lys	Cys	215	220	225	
Gly	Val	Gly	Val	Ala	Tyr	Asn	Ser	Lys	Val	Gly	Gly	Ile	Arg	Met	230	235	240	



**FIG. 3B**

Leu Asp Gly Ile	Val Thr Asp Ala Ile	Glu Ala Ser Ser Ile	Gly
245		250	255
Phe Asn Pro Gly	His Val Asp Ile Tyr	Ser Ala Ser Trp Gly	Pro
260		265	270
Asn Asp Asp Gly	Lys Thr Val Glu Gly	Pro Gly Arg Leu Ala	Gln
275		280	285
Lys Ala Phe Glu Tyr	Gly Val Lys Gln	Gly Arg Gln Gly Lys	Gly
290		295	300
Ser Ile Phe Val Trp	Ala Ser Gly Asn	Gly Gly Arg Gln Gly	Asp
305		310	315
Asn Cys Asp Cys Asp	Gly Tyr Thr Asp	Ser Ile Tyr Thr Ile	Ser
320		325	330
Ile Ser Ser Ala Ser	Gln Gln Gly Leu	Ser Pro Trp Tyr Ala	Glu
335		340	345
Lys Cys Ser Ser Thr	Leu Ala Thr Ser	Tyr Ser Ser Gly Asp	Tyr
350		355	360
Thr Asp Gln Arg Ile	Thr Ser Ala Asp	Leu His Asn Asp Cys	Thr
365		370	375
Glu Thr His Thr Gly	Thr Ser Ala Ser	Ala Pro Leu Ala Ala	Gly
380		385	390
Ile Phe Ala Leu Ala	Leu Glu Ala Asn	Pro Asn Leu Thr Trp	Arg
395		400	405
Asp Met Gln His Leu	Val Val Trp Thr	Ser Glu Tyr Asp Pro	Leu
410		415	420
Ala Ser Asn Pro Gly	Trp Lys Lys Asn	Gly Ala Gly Leu Met	Val
425		430	435
Asn Ser Arg Phe Gly	Phe Gly Leu Leu	Asn Ala Lys Ala Leu	Val
440		445	450
Asp Leu Ala Asp Pro	Arg Thr Trp Arg	Asn Val Pro Glu Lys	Lys
455		460	465
Glu Cys Val Val Lys	Asp Asn Asn Phe	Glu Pro Arg Ala Leu	Lys
470		475	480

## FIG. 3C

Ala	Asn	Gly	Glu	Val	Ile	Val	Glu	Ile	Pro	Thr	Arg	Ala	Cys	Glu	485	490	495
Gly	Gln	Glu	Asn	Ala	Ile	Lys	Ser	Leu	Glu	His	Val	Gln	Phe	Glu	500	505	510
Ala	Thr	Ile	Glu	Tyr	Ser	Arg	Arg	Gly	Asp	Leu	His	Val	Thr	Leu	515	520	525
Thr	Ser	Ala	Val	Gly	Thr	Ser	Thr	Val	Leu	Leu	Ala	Glu	Arg	Glu	530	535	540
Arg	Asp	Thr	Ser	Pro	Asn	Gly	Phe	Lys	Asn	Trp	Asp	Phe	Met	Ser	545	550	555
Val	His	Thr	Trp	Gly	Glu	Asn	Pro	Val	Gly	Thr	Trp	Thr	Leu	Lys	560	565	570
Ile	Thr	Asp	Met	Ser	Gly	Arg	Met	Gln	Asn	Glu	Gly	Arg	Ile	Val	575	580	585
Asn	Trp	Lys	Leu	Ile	Leu	His	Gly	Thr	Ser	Ser	Gln	Pro	Glu	His	590	595	600
Met	Lys	Gln	Pro	Arg	Val	Tyr	Thr	Ser	Tyr	Asn	Thr	Val	Gln	Asn	605	610	615
Asp	Arg	Arg	Gly	Val	Glu	Lys	Met	Val	Asn	Val	Val	Glu	Lys	Arg	620	625	630
Pro	Thr	Gln	Lys	Ser	Leu	Asn	Gly	Asn	Leu	Leu	Val	Pro	Lys	Asn	635	640	645
Ser	Ser	Ser	Ser	Asn	Val	Glu	Gly	Arg	Arg	Asp	Glu	Gln	Val	Gln	650	655	660
Gly	Thr	Pro	Ser	Lys	Ala	Met	Leu	Arg	Leu	Leu	Gln	Ser	Ala	Phe	665	670	675

## FIG. 3D

Ser	Lys	Asn	Ala	Leu	Ser	Lys	Gln	Ser	Pro	Lys	Lys	Ser	Pro	Ser
				680					685					690
Ala	Lys	Leu	Ser	Ile	Pro	Tyr	Glu	Ser	Phe	Tyr	Glu	Ala	Leu	Glu
				695					700					705
Lys	Leu	Asn	Lys	Pro	Ser	Lys	Leu	Glu	Gly	Ser	Glu	Asp	Ser	Leu
				710					715					720
Tyr	Ser	Asp	Tyr	Val	Asp	Val	Phe	Tyr	Asn	Thr	Lys	Pro	Tyr	Lys
				725					730					735
His	Arg	Asp	Asp	Arg	Leu	Leu	Gln	Ala	Leu	Met	Asp	Ile	Leu	Asn
				740					745					750
Glu	Glu	Asn												
		753												

## FIG. 4A

Met	Glu	Gly	Gly	Cys	Gly	Ser	Gln	Trp	Lys	Ala	Ala	Gly	Phe	Leu	1	5	10	15
Phe	Cys	Val	Met	Val	Phe	Ala	Ser	Ala	Glu	Arg	Pro	Val	Phe	Thr	20	25	30	
Asn	His	Phe	Leu	Val	Glu	Leu	His	Lys	Asp	Gly	Glu	Glu	Glu	Ala	35	40	45	
Arg	Gln	Val	Ala	Ala	Glu	His	Gly	Phe	Gly	Val	Arg	Lys	Leu	Pro	50	55	60	
Phe	Ala	Glu	Gly	Leu	Tyr	His	Phe	Tyr	His	Asn	Gly	Leu	Ala	Lys	65	70	75	
Ala	Lys	Arg	Arg	Ser	Leu	His	His	Lys	Arg	Gln	Leu	Glu	Arg		80	85	90	
Asp	Pro	Arg	Ile	Lys	Met	Ala	Leu	Gln	Gln	Glu	Gly	Phe	Asp	Arg	95	100	105	
Lys	Lys	Arg	Gly	Tyr	Arg	Asp	Ile	Asn	Glu	Ile	Asp	Ile	Asn	Met	110	115	120	
Asn	Asp	Pro	Leu	Phe	Thr	Lys	Gln	Trp	Tyr	Leu	Phe	Asn	Thr	Gly	125	130	135	
Gln	Ala	Asp	Gly	Thr	Pro	Gly	Leu	Asp	Leu	Asn	Val	Ala	Glu	Ala	140	145	150	
Trp	Glu	Leu	Gly	Tyr	Thr	Gly	Lys	Gly	Val	Thr	Ile	Gly	Ile	Met	155	160	165	

FIG. 4B

Asp	Asp	Gly	Ile	Asp	Tyr	Leu	His	Pro	Asp	Leu	Ala	Tyr	Asn	Tyr	180
				170					175						
Asn	Ala	Asp	Ala	Ser	Tyr	Asp	Phe	Ser	Ser	Asn	Asp	Pro	Tyr	Pro	195
				185					190						
Tyr	Pro	Arg	Tyr	Thr	Asp	Asp	Trp	Phe	Asn	Ser	His	Gly	Thr	Arg	210
				200					205						
Cys	Ala	Gly	Glu	Val	Ser	Ala	Ala	Ala	Ser	Asn	Asn	Ile	Cys	Gly	225
				215					220						
Val	Gly	Val	Ala	Tyr	Asn	Ser	Lys	Val	Ala	Gly	Ile	Arg	Met	Leu	240
				230					235						
Asp	Gln	Pro	Phe	Met	Thr	Asp	Ile	Ile	Glu	Ala	Ser	Ser	Ile	Ser	255
				245					250						
His	Met	Pro	Gln	Leu	Ile	Asp	Ile	Tyr	Ser	Ala	Ser	Trp	Gly	Pro	270
				260					265						
Thr	Asp	Asn	Gly	Lys	Thr	Val	Asp	Gly	Pro	Arg	Glu	Leu	Thr	Leu	285
				275					280						
Gln	Ala	Met	Ala	Asp	Gly	Val	Asn	Lys	Gly	Arg	Gly	Gly	Lys	Gly	
				290					295						300
Ser	Ile	Tyr	Val	Trp	Ala	Ser	Gly	Asp	Gly	Gly	Ser	Tyr	Asp	Asp	315
				305					310						
Cys	Asn	Cys	Asp	Gly	Tyr	Ala	Ser	Ser	Met	Trp	Thr	Ile	Ser	Ile	330
				320					325						

## FIG.4C

Asn Ser Ala Ile Asn Asp Gly Arg Thr Ala Leu Tyr Asp Glu Ser	335	340	345
Cys Ser Ser Thr Leu Ala Ser Thr Phe Ser Asn Gly Arg Lys Arg	350	355	360
Asn Pro Glu Ala Gly Val Ala Thr Thr Asp Leu Tyr Gly Asn Cys	365	370	375
Thr Leu Arg His Ser Gly Thr Ser Ala Ala Pro Glu Ala Ala	380	385	390
Gly Val Phe Ala Leu Ala Leu Glu Ala Asn Leu Asp Leu Thr Trp	395	400	405
Arg Asp Met Gln His Leu Thr Val Leu Thr Ser Lys Arg Asn Gln	410	415	420
Leu His Asp Glu Val His Gln Trp Arg Asn Gly Val Gly Leu	425	430	435
Glu Phe Asn His Leu Phe Gly Tyr Gly Val Leu Asp Ala Gly Ala	440	445	450
Met Val Lys Met Ala Lys Asp Trp Lys Thr Val Pro Glu Arg Phe	455	460	465
His Cys Val Gly Gly Ser Val Gln Asn Pro Glu Lys Ile Pro Pro	470	475	480
Thr Gly Lys Leu Val Leu Thr Leu Lys Thr Asn Ala Cys Glu Gly	485	490	495

**FIG.4D**

Lys Glu Asn Phe Val Arg Tyr Leu Glu His Val Gln Ala Val Ile	500	505	510
Thr Val Asn Ala Thr Arg Arg Gly Asp Leu Asn Ile Asn Met Thr	515	520	525
Ser Pro Met Gly Thr Lys Ser Ile Leu Leu Ser Arg Arg Pro Arg	530	535	540
Asp Asp Asp Ser Lys Val Gly Phe Asp Lys Trp Pro Phe Met Thr	545	550	555
Thr His Thr Trp Gly Glu Asp Ala Arg Gly Thr Trp Thr Leu Glu	560	565	570
Leu Gly Phe Val Gly Ser Ala Pro Gln Lys Gly Leu Leu Lys Glu	575	580	585
Trp Thr Leu Met Leu His Gly Thr Gln Ser Ala Pro Tyr Ile Asp	590	595	600
Gln Val Val Arg Asp Tyr Gln Ser Lys Leu Ala Met Ser Lys Lys	605	610	615
Gln Glu Leu Glu Glu Leu Asp Glu Ala Val Glu Arg Ser Leu	620	625	630
Gln Ser Ile Leu Arg Lys Asn	635	637	

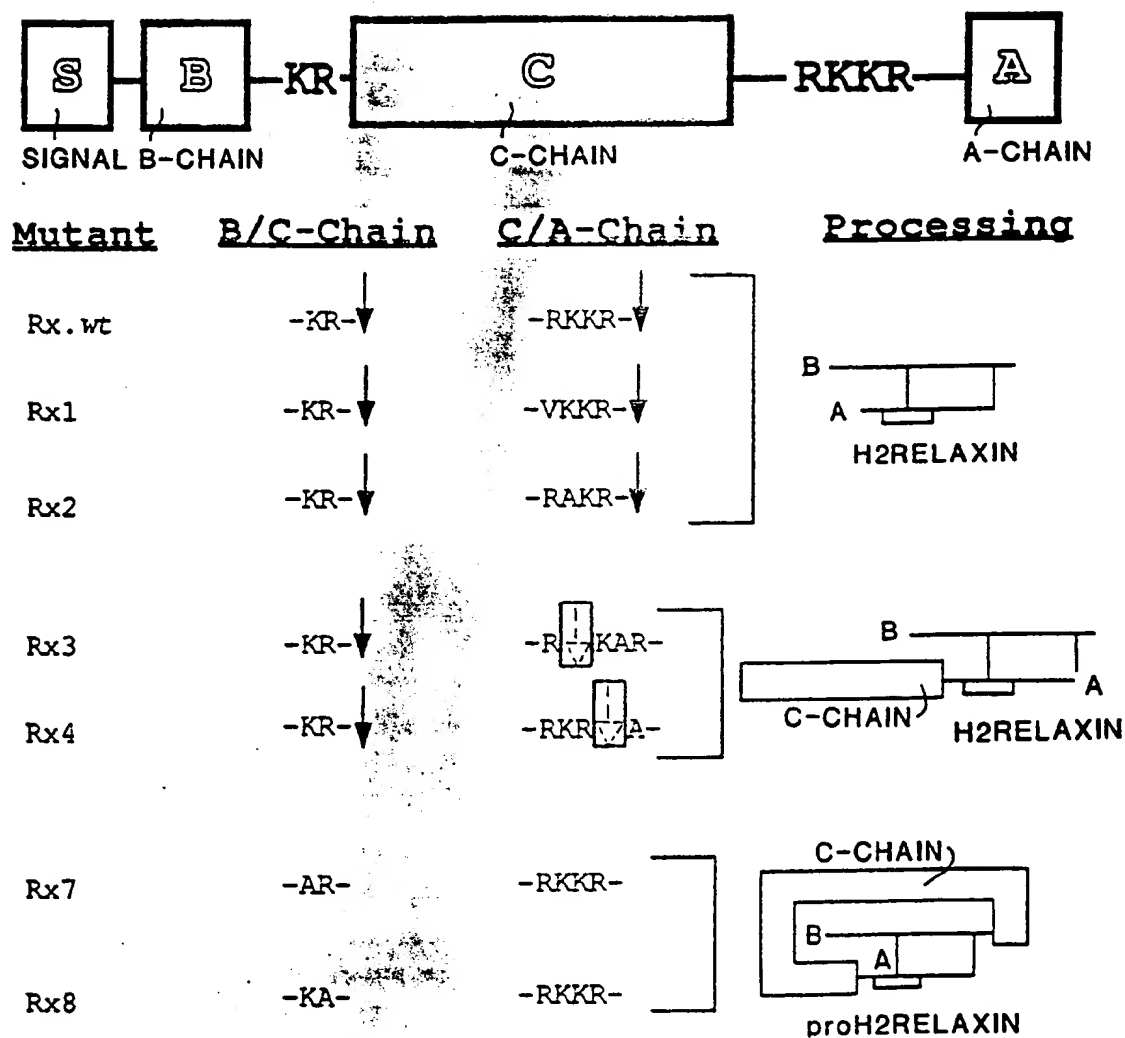


FIG. 5



PG1/US 92/10621

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III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		Relevant to Claim No.
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ANNEX TO THE INTERNATIONAL SEARCH REPORT  
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